



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 168291

**TO: Jeffrey Parkin
Location: REM-3D39/3C18
Art Unit: 1648
Monday, August 01, 2005
Case Serial Number: 10/085944**

**From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov**

Search Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

**Toby Port
X22523**

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160291

STIC-Biotech/ChemLib

From: Parkin, Jeffrey
Sent: Saturday, July 23, 2005 6:59 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search for U.S. Serial No. 10/085,944

Please search SEQ ID NOS.: 1 and 2 from the aforementioned application (U.S. Serial No. 10/085,944) v. all relevant databases. Place results on both paper and electronic format (i.e., disk, e-mail, etc.).

Thanks!

JSP
AU 1648
REM 3D39
2-0908

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM' nucleic - nucleic search, using sw model

Run on: July 31, 2005, 10:46:20 ; Search time 818 Seconds
(without alignments)
1658.614 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccattctcannatccctgctgttgg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

1: gb_ba.*
2: gb_btg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	25	89.3	339	14	AY612201 Dengue vi
C 2	25	89.3	339	14	AY612202 Dengue vi
C 3	25	89.3	339	14	AY612203 Dengue vi
C 4	25	89.3	339	14	AY612204 Dengue vi
C 5	25	89.3	339	14	AY612205 Dengue vi
C 6	25	89.3	339	14	AY612207 Dengue vi
C 7	25	89.3	339	14	AY612208 Dengue vi
C 8	25	89.3	2319	14	S66064
C 9	25	89.3	2325	14	AF469175 Dengue vi
C 10	25	89.3	2325	14	AF469176 Dengue vi
C 11	25	89.3	2357	6	AR232496 Sequence
C 12	25	89.3	2357	14	DEN2NGC
C 13	25	89.3	2552	14	AY152036S1
C 14	25	89.3	2552	14	AY152040S1
C 15	25	89.3	2552	14	AY152044S1
C 16	25	89.3	2552	14	AY152048S1
C 17	25	89.3	2552	14	AY152052S1
C 18	25	89.3	2552	14	AY152056S1
C 19	25	89.3	2552	14	AY152060S1

C 20	25	89.3	2552	14	AY152064S1	AY152064 Dengue vi
C 21	25	89.3	2552	14	AY152068S1	AY152068 Dengue vi
C 22	25	89.3	2552	14	AY152072S1	AY152072 Dengue vi
C 23	25	89.3	2552	14	AY152076S1	AY152076 Dengue vi
C 24	25	89.3	2552	14	AY152080S1	AY152080 Dengue vi
C 25	25	89.3	2552	14	AY152084S1	AY152084 Dengue vi
C 26	25	89.3	2552	14	AY152088S1	AY152088 Dengue vi
C 27	25	89.3	2552	14	AY152092S1	AY152092 Dengue vi
C 28	25	89.3	2552	14	AY152100S1	AY152100 Dengue vi
C 29	25	89.3	2552	14	AY152104S1	AY152104 Dengue vi
C 30	25	89.3	2552	14	AY152108S1	AY152108 Dengue vi
C 31	25	89.3	2552	14	AY152112S1	AY152112 Dengue vi
C 32	25	89.3	2552	14	AY152116S1	AY152116 Dengue vi
C 33	25	89.3	2552	14	AY152120S1	AY152120 Dengue vi
C 34	25	89.3	2552	14	AY152124S1	AY152124 Dengue vi
C 35	25	89.3	2552	14	AY152128S1	AY152128 Dengue vi
C 36	25	89.3	2552	14	AY152132S1	AY152132 Dengue vi
C 37	25	89.3	2552	14	AY152136S1	AY152136 Dengue vi
C 38	25	89.3	2552	14	AY152140S1	AY152144 Dengue vi
C 39	25	89.3	2552	14	AY152148S1	AY152148 Dengue vi
C 40	25	89.3	2552	14	AY152152S1	AY152152 Dengue vi
C 41	25	89.3	2552	14	AY152156S1	AY152156 Dengue vi
C 42	25	89.3	2552	14	AY152160S1	AY152160 Dengue vi
C 43	25	89.3	2552	14	AY152164S1	AY152164 Dengue vi
C 44	25	89.3	2552	14	AY152168S1	AY152168 Dengue vi
C 45	25	89.3	2552	14	AY152172S1	AY152172 Dengue vi
C 46	25	89.3	2552	14	AY152176S1	AY152176 Dengue vi
C 47	25	89.3	2552	14	AY152180S1	AY152180 Dengue vi
C 48	25	89.3	2552	14	AY152184S1	AY152184 Dengue vi
C 49	25	89.3	2552	14	AY152188S1	AY152188 Dengue vi
C 50	25	89.3	2552	14	AY152192S1	AY152192 Dengue vi
C 51	25	89.3	2552	14	AY152196S1	AY152196 Dengue vi
C 52	25	89.3	2552	14	AY152200S1	AY152200 Dengue vi
C 53	25	89.3	2552	14	AY152204S1	AY152204 Dengue vi
C 54	25	89.3	2552	14	AY152208S1	AY152208 Dengue vi
C 55	25	89.3	2552	14	AY152212S1	AY152212 Dengue vi
C 56	25	89.3	2552	14	AY152216S1	AY152216 Dengue vi
C 57	25	89.3	2552	14	AY152220S1	AY152220 Dengue vi
C 58	25	89.3	2552	14	AY152224S1	AY152224 Dengue vi
C 59	25	89.3	2552	14	AY152228S1	AY152228 Dengue vi
C 60	25	89.3	2552	14	AY152232S1	AY152232 Dengue vi
C 61	25	89.3	2552	14	AY152236S1	AY152236 Dengue vi
C 62	25	89.3	2552	14	AY152240S1	AY152240 Dengue vi
C 63	25	89.3	2552	14	AY152244S1	AY152244 Dengue vi
C 64	25	89.3	2552	14	AY152248S1	AY152248 Dengue vi
C 65	25	89.3	2552	14	AY152252S1	AY152252 Dengue vi
C 66	25	89.3	2552	14	AY152272S1	AY152272 Dengue vi
C 67	25	89.3	2552	14	AY152276S1	AY152276 Dengue vi
C 68	25	89.3	2552	14	AY152280S1	AY152280 Dengue vi
C 69	25	89.3	2552	14	AY152284S1	AY152284 Dengue vi
C 70	25	89.3	2552	14	AY152288S1	AY152288 Dengue vi
C 71	25	89.3	2552	14	AY152292S1	AY152292 Dengue vi
C 72	25	89.3	2552	14	AY152296S1	AY152296 Dengue vi
C 73	25	89.3	2552	14	AY152300S1	AY152300 Dengue vi
C 74	25	89.3	2552	14	AY152304S1	AY152304 Dengue vi
C 75	25	89.3	2552	14	AY152308S1	AY152308 Dengue vi
C 76	25	89.3	2552	14	AY152312S1	AY152312 Dengue vi
C 77	25	89.3	2552	14	AY152316S1	AY152316 Dengue vi
C 78	25	89.3	2552	14	AY152320S1	AY152320 Dengue vi
C 79	25	89.3	2552	14	AY152324S1	AY152324 Dengue vi
C 80	25	89.3	2552	14	AY152328S1	AY152328 Dengue vi
C 81	25	89.3	2552	14	AY152332S1	AY152332 Dengue vi
C 82	25	89.3	2552	14	AY152336S1	AY152336 Dengue vi
C 83	25	89.3	2552	14	AY152340S1	AY152340 Dengue vi
C 84	25	89.3	2552	14	AY152344S1	AY152344 Dengue vi
C 85	25	89.3	2552	14	AY152348S1	AY152348 Dengue vi
C 86	25	89.3	2552	14	AY152352S1	AY152352 Dengue vi
C 87	25	89.3	2552	14	AY152356S1	AY152356 Dengue vi
C 88	25	89.3	2552	14	AY152360S1	AY152360 Dengue vi
C 89	25	89.3	3381	14	DVU31949	U31949 Dengue viru
C 90	25	89.3	3381	14	DVU31950	U31950 Dengue viru
C 91	25	89.3	3381	14	DVU31951	U31951 Dengue viru
C 92	25	89.3	10597	14	DV1487271	AJ487271 Dengue vi

C 93	25	89.3	10618	14	AF326826	AF326826 Dengue vi	C 166	23.4	83.6	10648	6	AX224231	AX224231 Sequence
C 94	25	89.3	10618	14	AF326827	AF326827 Dengue vi	C 167	23.4	83.6	10648	6	AX224233	AX224233 Sequence
C 95	25	89.3	10648	14	DENSTRA	M14931 Dengue viru	C 168	23.4	83.6	10665	14	AF289029	AF289029 dengue vi
C 96	25	89.3	10649	14	AF326573	AF326573 Dengue vi	C 169	23.4	83.6	10674	14	AF100467	AF100467 Dengue vi
C 97	25	89.3	10649	14	AF326825	AF326825 Dengue vi	C 170	23.4	83.6	10674	14	AF100468	AF100468 Dengue vi
C 98	25	89.3	10649	14	AF326825	AF326825 Dengue vi	C 171	23.4	83.6	10684	14	AF100462	AF100462 Dengue vi
C 99	25	89.3	10682	14	AF375822	AF375822 Dengue vi	C 172	23.4	83.6	10722	14	AF489932	AF489932 Dengue vi
C 100	25	89.3	10685	14	AF100466	AF100466 Dengue vi	C 173	23.4	83.6	10723	14	AF022437	AF022437 Dengue vi
C 101	25	89.3	10685	14	AF100459	AF100459 Dengue vi	C 174	23.4	83.6	10723	14	AF022438	AF022438 Dengue vi
C 102	25	89.3	10685	14	AF100460	AF100460 Dengue vi	C 175	23.4	83.6	10723	14	AF022439	AF022439 Dengue vi
C 103	25	89.3	10685	14	AF100461	AF100461 Dengue vi	C 176	23.4	83.6	10723	14	AF119661	AF119661 Dengue vi
C 104	25	89.3	10685	14	AF100463	AF100463 Dengue vi	C 177	23.4	83.6	10723	14	M20558	Dengue viru
C 105	25	89.3	10717	6	AX224217	AX224217 Sequence	C 178	23.4	83.6	10723	14	AF593218	AF593218 Dengue vi
C 106	25	89.3	10723	6	AX224219	AX224219 Sequence	C 179	21.8	77.9	350	14	AF593219	AF593219 Dengue vi
C 107	25	89.3	10723	6	AX224221	AX224221 Sequence	C 180	21.8	77.9	350	14	AF593220	AF593220 Dengue vi
C 108	25	89.3	10723	6	AX224223	AX224223 Sequence	C 181	21.8	77.9	350	14	AF593221	AF593221 Dengue vi
C 109	25	89.3	10723	6	AX224235	AX224235 Sequence	C 182	21.8	77.9	350	14	AF593222	AF593222 Dengue vi
C 110	25	89.3	10723	14	AF022435	AF022435 Dengue vi	C 183	21.8	77.9	350	14	AF593223	AF593223 Dengue vi
C 111	25	89.3	10723	14	AF022436	AF022436 Dengue vi	C 184	21.8	77.9	350	14	AF593224	AF593224 Dengue vi
C 112	25	89.3	10723	14	AF022440	AF022440 Dengue vi	C 185	21.8	77.9	350	14	AF593225	AF593225 Dengue vi
C 113	25	89.3	10723	14	AF022441	AF022441 Dengue vi	C 186	21.8	77.9	350	14	AF593226	AF593226 Dengue vi
C 114	25	89.3	10723	14	AF169678	AF169678 Dengue vi	C 187	21.8	77.9	350	14	AF593227	AF593227 Dengue vi
C 115	25	89.3	10723	14	AF169679	AF169679 Dengue vi	C 188	21.8	77.9	350	14	AF593228	AF593228 Dengue vi
C 116	25	89.3	10723	14	AF169680	AF169680 Dengue vi	C 189	21.8	77.9	366	14	AF047401	Dengue vi
C 117	25	89.3	10723	14	AF169681	AF169681 Dengue vi	C 190	21.8	77.9	367	14	AF047393	AF047393 Dengue vi
C 118	25	89.3	10723	14	AF169682	AF169682 Dengue vi	C 191	21.8	77.9	376	14	AF047395	AF047395 Dengue vi
C 119	25	89.3	10723	14	AF169683	AF169683 Dengue vi	C 192	21.8	77.9	400	14	AF324614	Dengue vi
C 120	25	89.3	10723	14	AF169684	AF169684 Dengue vi	C 193	21.8	77.9	400	14	AF324615	Dengue vi
C 121	25	89.3	10723	14	AF169685	AF169685 Dengue vi	C 194	21.8	77.9	400	14	AF324616	Dengue vi
C 122	25	89.3	10723	14	AF169686	AF169686 Dengue vi	C 195	21.8	77.9	400	14	AF324617	Dengue vi
C 123	25	89.3	10723	14	AF169687	AF169687 Dengue vi	C 196	21.8	77.9	400	14	AF324618	Dengue vi
C 124	25	89.3	10723	14	AF169688	AF169688 Dengue vi	C 197	21.8	77.9	400	14	AF324619	Dengue vi
C 125	25	89.3	10723	14	AF204177	AF204177 Dengue vi	C 198	21.8	77.9	400	14	AF324620	Dengue vi
C 126	25	89.3	10723	14	AF204178	AF204178 Dengue vi	C 199	21.8	77.9	400	14	AF324621	Dengue vi
C 127	25	89.3	10723	14	DENCCGA	M29095 Dengue viru	C 200	21.8	77.9	400	14	AF324622	Dengue vi
C 128	25	89.3	10723	14	DENCMEMSA	M84728 Dengue viru	C 201	21.8	77.9	400	14	AF324623	Dengue vi
C 129	25	89.3	10723	14	DENCMEMSB	M84727 Dengue viru	C 202	21.8	77.9	400	14	AF324624	Dengue vi
C 130	25	89.3	10723	14	U87411	U87411 Dengue viru	C 203	21.8	77.9	403	14	AF047398	AF047398 Dengue vi
C 131	25	89.3	10723	14	U87412	U87412 Dengue viru	C 204	21.8	77.9	405	14	AF047396	Dengue vi
C 132	25	89.3	10724	14	AF022434	AF022434 Dengue vi	C 205	21.8	77.9	406	14	AF047394	Dengue vi
C 133	25	89.3	10724	14	AF038402	AF038402 Dengue vi	C 206	21.8	77.9	406	14	AF047397	Dengue vi
C 134	25	89.3	10724	14	AF038403	AF038403 Dengue vi	C 207	21.8	77.9	406	14	AF047400	Dengue vi
C 135	25	89.3	10756	6	AX224225	AX224225 Sequence	C 208	21.8	77.9	406	14	AF047402	Dengue vi
C 136	25	89.3	15237	12	AY243469	AY243469 Chimeric	C 209	21.8	77.9	454	14	AF177541	Dengue vi
C 137	25	89.3	15239	12	AY243467	AY243467 Chimeric	C 210	21.8	77.9	454	14	AF706095	AF706095 Dengue vi
C 138	25	89.3	15239	12	AY376438	AY376438 Dengue vi	C 211	21.8	77.9	840	14	AF360860	Dengue vi
C 139	25	89.3	15256	12	AY656168	AY656168 Chimeric	C 212	21.8	77.9	840	14	AF360861	Dengue vi
C 140	25	89.3	15268	12	AY243468	AY243468 Chimeric	C 213	21.8	77.9	2325	14	AF509530	AF509530 Dengue vi
C 141	25	89.3	15270	12	AY243466	AY243466 Chimeric	C 214	21.8	77.9	2474	14	DENTAH	D00502 Dengue viru
C 142	25	89.3	15270	12	AY648301	AY648301 Dengue vi	C 215	21.8	77.9	3381	6	AR122077	AR122077 Sequence
C 143	25	89.3	15287	12	AY656167	AY656167 Chimeric	C 216	21.8	77.9	3381	6	AR122078	AR122078 Sequence
C 144	23.4	83.6	339	14	AY612206	AY612206 Dengue vi	C 217	21.8	77.9	3381	6	AR135737	AR135737 Sequence
C 145	23.4	83.6	342	14	FLD3CPM1	X51708 Dengue-2 vi	C 218	21.8	77.9	3381	6	AR135738	AR135738 Sequence
C 146	23.4	83.6	342	14	FLD3CPM2	X51709 Dengue-2 vi	C 219	21.8	77.9	3381	6	AR559088	AR559088 Sequence
C 147	23.4	83.6	342	14	FLD3CPM3	X51710 Dengue-2 vi	C 220	21.8	77.9	3381	6	BD073455	BD073455 Recombina
C 148	23.4	83.6	351	14	AY079176	AY079176 Dengue vi	C 221	21.8	77.9	3381	14	DVU88237	DVU88237 Dengue viru
C 149	23.4	83.6	406	14	AF047399	AF047399 Dengue vi	C 222	21.8	77.9	10674	14	AF100465	AF100465 Dengue vi
C 150	23.4	83.6	454	14	AF177542	AF177542 Dengue vi	C 223	21.8	77.9	10674	14	AF100469	Dengue vi
C 151	23.4	83.6	454	14	AF706094	AF706094 Dengue vi	C 224	21.8	77.9	10703	14	DENRCG	M19397 Dengue viru
C 152	23.4	83.6	475	14	DEN3CPMP	274048 Dengue viru	C 225	21.8	77.9	10722	14	AF208496	AF208496 Dengue vi
C 153	23.4	83.6	840	14	AF360862	AF360862 Dengue vi	C 226	21.8	77.9	10723	14	AB122020	AB122020 Dengue vi
C 154	23.4	83.6	840	14	AF360863	AF360863 Dengue vi	C 227	21.8	77.9	10723	14	AB122021	Dengue vi
C 155	23.4	83.6	2325	14	AY044442	AY044442 Dengue vi	C 228	21.8	77.9	10723	14	AB122022	Dengue vi
C 156	23.4	83.6	2469	14	DENTAMA	M15075 Dengue viru	C 229	21.8	77.9	10723	14	AB189122	Dengue vi
C 157	23.4	83.6	2552	14	AY152096S1	AY152096 Dengue vi	C 230	21.8	77.9	10723	14	AB189123	Dengue vi
C 158	23.4	83.6	2552	14	AY152140S1	AY152140 Dengue vi	C 231	21.8	77.9	10723	14	AB189124	Dengue vi
C 159	23.4	83.6	2552	14	AY152256S1	AY152256 Dengue vi	C 232	21.8	77.9	10723	14	AF276619	AF276619 Dengue vi
C 160	23.4	83.6	2552	14	AY152260S1	AY152260 Dengue vi	C 233	21.8	77.9	10723	14	AF359579	AF359579 Dengue vi
C 161	23.4	83.6	2552	14	AY152264S1	AY152264 Dengue vi	C 234	21.8	77.9	10723	14	AY037116	Dengue vi
C 162	23.4	83.6	2552	14	AY152268S1	AY152268 Dengue vi	C 235	20.2	72.1	342	14	DEN2CPG	X65239 Dengue-2 vi
C 163	23.4	83.6	3381	14	DVU31952	U31952 Dengue viru	C 236	20.2	72.1	342	14	DV1CAPSID	X70952 Dengue viru
C 164	23.4	83.6	3381	14	DVU89517	U89517 Dengue viru	C 237	20.2	72.1	364	14	AY584591	Dengue vi
C 165	23.4	83.6	3381	14	DVU89518	U89518 Dengue viru	C 238	20.2	72.1	364	14	AY584592	Dengue vi

C 239	20.2	72.1	364	14	AY5845593	AY5845593 Dengue vi	C 312	19.2	68.6	2887	14	AY277654	Dengue vi
C 240	20.2	72.1	364	14	AY5845594	AY5845594 Dengue vi	C 313	19.2	68.6	2887	14	AY277655	Dengue vi
C 241	20.2	72.1	364	14	AY6121195	AY6121195 Dengue vi	C 314	19.2	68.6	2887	14	AY277656	Dengue vi
C 242	20.2	72.1	364	14	AY6121196	AY6121196 Dengue vi	C 315	19.2	68.6	2887	14	AY277657	Dengue vi
C 243	20.2	72.1	364	14	AY6121198	AY6121198 Dengue vi	C 316	19.2	68.6	2887	14	AY277658	Dengue vi
C 244	20.2	72.1	364	14	AY6122000	AY6122000 Dengue vi	C 317	19.2	68.6	2887	14	AY277659	Dengue vi
C 245	20.2	72.1	426	14	AF5380208	AF5380208 Dengue vi	C 318	19.2	68.6	2887	14	AY277660	Dengue vi
C 246	20.2	72.1	436	14	AF538023	AF538023 Dengue vi	C 319	19.2	68.6	2887	14	AY277661	Dengue vi
C 247	20.2	72.1	483	14	AF538031	AF538031 Dengue vi	C 320	19.2	68.6	2887	14	AY277662	Dengue vi
C 248	20.2	72.1	491	14	AF538030	AF538030 Dengue vi	C 321	19.2	68.6	2887	14	AY277663	Dengue vi
C 249	20.2	72.1	493	14	AF538024	AF538024 Dengue vi	C 322	19.2	68.6	10721	14	AF298807	Dengue vi
C 250	20.2	72.1	497	14	AF538027	AF538027 Dengue vi	C 323	19.2	68.6	10735	14	AB074761	Dengue vi
C 251	20.2	72.1	501	14	AF538025	AF538025 Dengue vi	C 324	19.2	68.6	10735	14	AF226685	Dengue vi
C 252	20.2	72.1	501	14	AF538026	AF538026 Dengue vi	C 325	19.2	68.6	10735	14	AF226686	Dengue vi
C 253	20.2	72.1	502	14	AF538029	AF538029 Dengue vi	C 326	19.2	68.6	10735	14	AF226687	Dengue vi
C 254	20.2	72.1	506	14	DEN1CMP	774047 Dengue viru	C 327	19.2	68.6	10735	14	AF311956	Dengue vi
C 255	20.2	72.1	960	14	S755335	S755335 Dengue viru	C 328	19.2	68.6	10735	14	AF311957	Dengue vi
C 256	20.2	72.1	2419	14	DENPPSP	L04561 Dengue viru	C 329	19.2	68.6	10735	14	AF311958	Dengue vi
C 257	20.2	72.1	2461	14	DENP83	D00503 Dengue viru	C 330	19.2	68.6	10735	14	AF513110	Dengue vi
C 258	20.2	72.1	3745	14	DEN1EWNS	M23027 Dengue viru	C 331	19.2	68.6	10735	14	AF514876	Dengue vi
C 259	20.2	72.1	10014	14	AY373427	AY373427 Dengue vi	C 332	19.2	68.6	10735	14	AF514878	Dengue vi
C 260	20.2	72.1	10014	14	AY376738	AY376738 Dengue vi	C 333	19.2	68.6	10735	14	AF514883	Dengue vi
C 261	20.2	72.1	10705	14	AY145123	AY145123 Dengue vi	C 334	19.2	68.6	10735	14	AF514885	Dengue vi
C 262	20.2	72.1	10717	14	DENT1SEQ	M87512 Dengue viru	C 335	19.2	68.6	10735	14	AF514889	Dengue vi
C 263	20.2	72.1	10718	6	A75711	A75711 Sequence 1	C 336	19.2	68.6	10735	14	AY206457	Dengue vi
C 264	20.2	72.1	10718	6	E06832	E06832 DNA sequenc	C 337	19.2	68.6	10735	14	AY277665	Dengue vi
C 265	20.2	72.1	10721	14	AF298808	AF298808 Dengue vi	C 338	19.2	68.6	10735	14	AY277666	Dengue vi
C 266	20.2	72.1	10721	14	AF309641	AF309641 Dengue vi	C 339	19.2	68.6	10735	14	AY277666	Dengue vi
C 267	20.2	72.1	10723	6	AX224213	AX224213 Sequence	C 340	19.2	68.6	110000	2	AC096436	Rattus no
C 268	20.2	72.1	10723	6	AX224215	AX224215 Sequence	C 341	19.2	68.6	115431	9	AC010880	Homo sapi
C 269	20.2	72.1	10733	14	AY145122	AY145122 Dengue vi	C 342	19.2	68.6	143687	9	AC016572	Homo sapi
C 270	20.2	72.1	10735	6	AX224209	AX224209 Sequence	C 343	19.2	68.6	146078	9	AC091874	Homo sapi
C 271	20.2	72.1	10735	6	AX224211	AX224211 Sequence	C 344	19.2	68.6	149082	2	AP005867	Oryza sat
C 272	20.2	72.1	10735	14	AB074760	AB074760 Dengue vi	C 345	19.2	68.6	157415	8	AP005867	Oryza sat
C 273	20.2	72.1	10735	14	AB178040	AB178040 Dengue vi	C 346	19.2	68.6	158842	8	AC136491	Human DNA
C 274	20.2	72.1	10735	14	AB189120	AB189120 Dengue vi	C 347	19.2	68.6	169897	9	AL353674	Oryza sat
C 275	20.2	72.1	10735	14	AB189121	AB189121 Dengue vi	C 348	19.2	68.6	181444	9	AC104299	Homo sapi
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C 280	20.2	72.1	10735	14	DVU88535	U88535 Dengue viru	C 353	19.2	68.6	219391	2	AC123146	Rattus no
C 281	20.2	72.1	10735	14	DVU88537	U88536 Dengue viru	C 354	19.2	68.6	219477	10	AC123838	Mus muscu
C 282	20.2	72.1	10735	14	DVU88537	U88537 Dengue viru	C 355	19.2	68.6	233864	10	AC122860	Mus muscu
C 283	20.2	72.1	164266	5	BX321906	BX321906 Zebrafish	C 356	18.8	67.1	2237	6	CQ877114	Sequence
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C 286	19.8	70.7	169082	10	AC130538	AC130538 Mus muscu	C 359	18.8	67.1	5674	6	AR153499	Sequence
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C 289	19.4	69.3	89880	8	AC149306	AC149306 Medicago	C 362	18.8	67.1	5674	6	AR268060	Sequence
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C 293	19.4	69.3	329457	2	AC103339	AC103339 Rattus no	C 366	18.8	67.1	43248	9	BS000044	Pan trogl
C 294	19.2	68.6	333	14	AF514882	AF514882 Dengue vi	C 367	18.8	67.1	131414	9	HSF10238	Human DNA
C 295	19.2	68.6	333	14	AF514884	AF514884 Dengue vi	C 368	18.8	67.1	146715	9	AL355795	Human DNA
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C 301	19.2	68.6	364	14	AY593212	AY593212 Dengue vi	C 374	18.8	67.1	192370	2	AC016857	Homo sapi
C 302	19.2	68.6	364	14	AY593213	AY593213 Dengue vi	C 375	18.8	67.1	194074	9	AC090095	Homo sapi
C 303	19.2	68.6	364	14	AY593214	AY593214 Dengue vi	C 376	18.8	67.1	195270	9	AC096534	Homo sapi
C 304	19.2	68.6	364	14	AY593215	AY593215 Dengue vi	C 377	18.8	67.1	199810	9	AC018443	Homo sapi
C 305	19.2	68.6	364	14	AY593216	AY593216 Dengue vi	C 378	18.8	67.1	2590029	9	U82670	Homo sapien
C 306	19.2	68.6	364	14	AY593217	AY593217 Dengue vi	C 379	18.8	67.1	300029	8	AE017105	Oryza sat
C 307	19.2	68.6	479	14	AY079173	AY079173 Dengue vi	C 380	18.8	66.4	241	14	AY331409	Dengue vi
C 308	19.2	68.6	2325	14	S64849	S64849 C...E (deng	C 381	18.6	66.4	241	14	AY331409	Dengue vi
C 309	19.2	68.6	2474	14	DENCCV	D00501 Dengue viru	C 382	18.6	66.4	241	14	AY331412	Dengue vi
C 310	19.2	68.6	2887	14	AY277652	AY277652 Dengue vi	C 383	18.6	66.4	290	14	AY079175	Dengue vi
C 311	19.2	68.6	2887	14	AY277653	AY277653 Dengue vi	C 384	18.6	66.4	318	14	AF495889	Dengue vi

C 385	18.6	66.4	318	14	AF495890	Dengue vi	AF495890	Dengue vi	C 458	18.6	66.4	1050	14	AB010987	Dengue vi
C 386	18.6	66.4	318	14	AF495891	Dengue vi	AF495891	Dengue vi	C 459	18.6	66.4	1050	14	AB010988	Dengue vi
C 387	18.6	66.4	318	14	AF495892	Dengue vi	AF495892	Dengue vi	C 460	18.6	66.4	1050	14	AB010989	Dengue vi
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C 395	18.6	66.4	318	14	AF495900	Dengue vi	AF495900	Dengue vi	C 468	18.6	66.4	1050	14	AB038471	Dengue vi
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C 403	18.6	66.4	364	14	AY612197	Dengue vi	AY612197	Dengue vi	C 476	18.6	66.4	1050	14	AB038479	Dengue vi
C 404	18.6	66.4	364	14	AY612199	Dengue vi	AY612199	Dengue vi	C 477	18.6	66.4	1923	14	AY665402	Dengue vi
C 405	18.6	66.4	453	14	AY706096	Dengue vi	AY706096	Dengue vi	C 478	18.6	66.4	2297	14	DENENVA	Dengue vi
C 406	18.6	66.4	454	14	AY706097	Dengue vi	AY706097	Dengue vi	C 479	18.6	66.4	2300	6	AX653068	Sequence
C 407	18.6	66.4	454	14	AY706099	Dengue vi	AY706099	Dengue vi	C 480	18.6	66.4	2880	14	AY099338S1	Dengue vi
C 408	18.6	66.4	455	14	AY706098	Dengue vi	AY706098	Dengue vi	C 481	18.6	66.4	2880	14	AY099339S1	Dengue vi
C 409	18.6	66.4	486	6	CO110182	Sequence	CO110182	Sequence	C 482	18.6	66.4	2880	14	AY099340S1	Dengue vi
C 410	18.6	66.4	486	6	CO148890	Sequence	CO148890	Sequence	C 483	18.6	66.4	2880	14	AY099341S1	Dengue vi
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C 412	18.6	66.4	486	6	CO270269	Sequence	CO270269	Sequence	C 485	18.6	66.4	3424	3	AF217250	Helicover
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C 414	18.6	66.4	486	6	CO344347	Sequence	CO344347	Sequence	C 487	18.6	66.4	10707	14	AY099336	Dengue vi
C 415	18.6	66.4	495	14	AF008555	Dengue vi	AF008555	Dengue vi	C 488	18.6	66.4	10707	14	AY099337	Dengue vi
C 416	18.6	66.4	495	14	AF547236	Dengue vi	AF547236	Dengue vi	C 489	18.6	66.4	10707	14	AY099338	Dengue vi
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C 418	18.6	66.4	495	14	AF547238	Dengue vi	AF547238	Dengue vi	C 491	18.6	66.4	14364	1	AF498415	Pseudomon
C 419	18.6	66.4	495	14	AF547239	Dengue vi	AF547239	Dengue vi	C 492	18.6	66.4	40516	9	AL807750	Gibbon DN
C 420	18.6	66.4	495	14	AF547240	Dengue vi	AF547240	Dengue vi	C 493	18.6	66.4	40565	2	AL731848	Hylobates
C 421	18.6	66.4	495	14	AF547241	Dengue vi	AF547241	Dengue vi	C 494	18.6	66.4	51536	9	AC100760	Homo sapi
C 422	18.6	66.4	495	14	AF547242	Dengue vi	AF547242	Dengue vi	C 495	18.6	66.4	51574	2	AC138651	Homo sapi
C 423	18.6	66.4	495	14	AF547243	Dengue vi	AF547243	Dengue vi	C 496	18.6	66.4	51720	2	AC027294	Continuation (5 of
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C 426	18.6	66.4	495	14	AF547246	Dengue vi	AF547246	Dengue vi	C 499	18.6	66.4	66330	2	AC135261	Homo sapi
C 427	18.6	66.4	495	14	AF547247	Dengue vi	AF547247	Dengue vi	C 500	18.6	66.4	66330	2	AC125619	Continuation (3 of
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C 454	18.6	66.4	495	14	AF547274	Dengue vi	AF547274	Dengue vi				110000	2		
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C 456	18.6	66.4	495	14	AF547276	Dengue vi	AF547276	Dengue vi				110000	2		
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ALIGNMENTS

RESULT 1	AY612201/c	339 bp	RNA	linear	VRL 06-OCT-2004
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DEFINITION	Dengue virus type 1 isolate 22/99/thailand polypeptide gene,				
ACCESSION	AY612201				
VERSION	AY612201.1				
KEYWORDS	Dengue virus type 1				
SOURCE	Dengue virus type 1				
ORGANISM	Dengue virus type 1				
REFERENCE	1 (bases 1 to 339)				
AUTHORS	Urvaashi S.B., Yokan S., Sunita K. and Seth P.				
TITLE	Dengue virus evolution in India and Thailand				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 339)				
AUTHORS	Urvaashi S.B., Yokan S., Sunita K. and Seth P.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-APR-2004) Microbiology, All India Institute of				
FEATURES	Medical Sciences, Aneari Nagar, New Delhi 110 029, India				
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RESULT 3
AY612203/c
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ACCESSION
AY612203
VERSION
AY612203.1
KEYWORDS
GI:53680720
SOURCE
Dengue virus type 2
ORGANISM
Dengue virus type 2
REFERENCE
1 (bases 1 to 339)
Urvashi,S.B., Yokean,S., Sunita,K. and Seth,P.
Dengue virus evolution in India and Thailand
Unpublished
2 (bases 1 to 339)
Urvashi,S.B., Yokean,S., Sunita,K. and Seth,P.
Direct Submission
Submitted (29-APR-2004) Microbiology, All India Institute of Medical Sciences, Ansari Nagar, New Delhi 110 029, India
Location/Qualifiers
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCATCTCTCANNATCCCTGCTGTTGG 28
|||||
DB 79 CCCATCTCTTCAATATCCCTGCTGTTGG 52

RESULT 4
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LOCUS
DEFINITION
Dengue virus type 2 isolate 8/91/thailand polyprotein gene, partial cds.
ACCESSION
AY612204
VERSION
AY612204.1
KEYWORDS
GI:53680722
SOURCE
Dengue virus type 2
ORGANISM
Dengue virus type 2
REFERENCE
1 (bases 1 to 339)
Urvashi,S.B., Yokean,S., Sunita,K. and Seth,P.
Dengue virus evolution in India and Thailand
Unpublished
2 (bases 1 to 339)
Urvashi,S.B., Yokean,S., Sunita,K. and Seth,P.
Direct Submission
Submitted (29-APR-2004) Microbiology, All India Institute of Medical Sciences, Ansari Nagar, New Delhi 110 029, India
Location/Qualifiers
1. .339
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NMCTLMAMDIG"
ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCATCTCTCANNATCCCTGCTGTTGG 28
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DB 79 CCCATCTCTTCAATATCCCTGCTGTTGG 52
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/mol_type="genomic RNA"
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ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

RESULT 5
AY612205/c
LOCUS      339 bp      RNA      linear      VRL 06-OCT-2004
DEFINITION Dengue virus type 2 isolate 91/91/thailand polyprotein gene,
partial cds.
ACCESSION  AY612205
VERSION     AY612205.1
KEYWORDS    Dengue virus type 2
ORGANISM    Dengue virus type 2
REFERENCE   1 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Dengue virus evolution in India and Thailand
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-2004) Microbiology, All India Institute of
Medical Sciences, Ansari Nagar, New Delhi 110 029, India
FEATURES    Location/Qualifiers
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ORIGIN
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Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

RESULT 6
AY612207/c
LOCUS      339 bp      RNA      linear      VRL 06-OCT-2004
DEFINITION Dengue virus type 2 isolate T627/thailand polyprotein gene, partial
cds.
ACCESSION  AY612207
VERSION     AY612207.1
KEYWORDS    Dengue virus type 2
ORGANISM    Dengue virus type 2
REFERENCE   1 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Dengue virus evolution in India and Thailand
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-2004) Microbiology, All India Institute of
Medical Sciences, Ansari Nagar, New Delhi 110 029, India
FEATURES    Location/Qualifiers
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             /protein_id="AAU89555.1"
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             NMCTLMKPDG"

ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

RESULT 7
AY612208/c
LOCUS      339 bp      RNA      linear      VRL 06-OCT-2004
DEFINITION Dengue virus type 2 isolate T7/thailand polyprotein gene, partial
cds.
ACCESSION  AY612208
VERSION     AY612208.1
KEYWORDS    Dengue virus type 2
ORGANISM    Dengue virus type 2
REFERENCE   1 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Dengue virus evolution in India and Thailand
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 339)
AUTHORS     Urvaashi,S.B., Yoksan,S., Sunita,K. and Seth,P.
TITLE       Direct Submission
JOURNAL     Submitted (29-APR-2004) Microbiology, All India Institute of
Medical Sciences, Ansari Nagar, New Delhi 110 029, India
FEATURES    Location/Qualifiers
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             NMCTLMAMDLG"

ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 79 CCCATCTCTTCATATCCCTGCTGTGG 52

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/serotype="2"
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/db_xref="taxon:11060"
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NMCTLMAMDIG"

CDS
Query Match      89.3%; Score 25; DB 14; Length 339;
Best Local Similarity 89.3%; Pred. No. 1.3;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTTCANNATCCCTGCTGTGG 28
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Db 79 CCATCTCTTCAATATCCCTGCTGTGG 52

RESULT 8
S66064/c
LOCUS      2319 bp DNA linear VRL 04-DEC-1993
DEFINITION structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt].
ACCESSION S66064.1 GI:432575
VERSION   1
KEYWORDS  Dengue virus type 4
SOURCE    Dengue virus type 4
ORGANISM  Dengue virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2319)
AUTHORS   Kawano,H., Rostapahov,V., Rosen,L. and Lai,C.J.
TITLE     Genetic determinants of dengue type 4 virus neurovirulence for mice
JOURNAL   J. Virol. 67 (11), 6567-6575 (1993)
MEDLINE   94016840
PUBMED    8411360
REMARK    GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138430] from the original journal article.

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EVLKPDGEULTDCPRSGIDFNEMILMKKKTLWLHVKQWFLDPLPMPAAGADTSEV
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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTTCANNATCCCTGCTGTGG 28
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Db 205 CCATCTCTTCAGATCCCTGCTGTGG 178

RESULT 9
AF469175/c
LOCUS      2325 bp RNA linear VRL 20-FEB-2002
DEFINITION Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
ACCESSION AF469175
VERSION   1
KEYWORDS  Dengue virus type 2
SOURCE    Dengue virus type 2
ORGANISM  Dengue virus type 2
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2325)
AUTHORS   Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE     Structural genes of dengue virus type 2 strain GD24/93 isolate from
            Nanhai, Guangdong, China
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 2325)
AUTHORS   Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
            Zhao,W.Z.
TITLE     Direct Submission
JOURNAL   Submitted (16-JAN-2002) Department of Virology, The Military
            Medical Institute of Guangzhou Military District, Dong Guanzhuang
            Road 91, Guangzhou, Guangdong 5105407, China

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TRTETWMSSEGAWKHAQRJETWILRHPGPTMAAILAYTIGTHFORALIFILLTAVA
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ORIGIN
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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTTCANNATCCCTGCTGTGG 28
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Db 208 CCATCTCTTCAATATCCCTGCTGTGG 181
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ORIGIN

RESULT 10
AF469176/c 2325 bp RNA linear VRL 20-FEB-2002
LOCUS
DEFINITION Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
ACCESSION AF469176
VERSION AF469176.1 GI:18766556
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
Unpublished
2 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
Zhao,W.Z.
Direct Submission
Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
Location/Qualifiers
1. .2325
/organism="Dengue virus type 2"
/mol_type="genomic RNA"
/strain="GD08/98"
/db_xref="taxon:11060"
/country="China: Nanhai, Guangdong province"
/note="isolated from dengue haemorrhagic fever patient"

CDS
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PSMTMRCIGISNRDFVSGSGSWDIVLEHSGCVTTMAKNKPTLDFELIKTEAKQPA
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ORIGIN
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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 208 CCCATCTCTCAATATCCCTGCTGTTGG 181

RESULT 11
AR232496/c 2357 bp RNA linear PAT 20-DEC-2002
LOCUS
DEFINITION Sequence 1 from patent US 6455509.
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unclassified.

ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2325;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 208 CCCATCTCTCAATATCCCTGCTGTTGG 181

ORIGIN
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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

ORIGIN
Query Match 89.3%; Score 25; DB 6; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

REFERENCE
AUTHORS Kocheil,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
TITLE Dengue nucleic acid vaccines that induce neutralizing antibodies
JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
1. .2357
/organism="unknown"
/mol_type="genomic RNA"

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Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

RESULT 12
DEN2NGC/c 2357 bp RNA linear VRL 29-MAY-2002
LOCUS
DEFINITION Dengue virus type 2 gene for polyprotein, partial cds, strain:New
Guinea C.
ACCESSION D00346
VERSION D00346.1 GI:221230
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2357)
Gruenberg,A., Woo,W.S., Biedrzycka,A. and Wright,P.J.
Partial nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue virus type 2, New Guinea C and
PUO-218 strains
J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
88258474
3385407

ORIGIN
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Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

ORIGIN
Query Match 89.3%; Score 25; DB 6; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

ORIGIN
Query Match 89.3%; Score 25; DB 6; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

ORIGIN
Query Match 89.3%; Score 25; DB 6; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.98;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
Db 228 CCCATCTCTTCAATATCCCTGCTGTTGG 201

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Db 228 CCATCTCTCAGTATCCCTGCTGTGG 201

RESULT 13
AY152036S1/c 2552 bp RNA linear VRL 29-SEP-2003
LOCUS Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
           Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
           Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
           Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 14
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LOCUS Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152040
VERSION AY152040.1 GI:28170815
KEYWORDS
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
           Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
           Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
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ORIGIN
Query Match 89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCANTCANNATCCCTGCTGTGG 28
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Db 205 CCATCTCTCAGATCCCTGCTGTGG 178
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DEFINITION Dengue virus type 4 D4.18_1998 polyprotein precursor, gene, partial
cde.
ACCESSION AY152044
VERSION AY152044.1 GI:28170824
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
PUBLISHED
JOURNAL
TITLE
AUTHORS
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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Best Local Similarity 89.3%; Pred. No. 0.97;
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Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTGG 178
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LOCUS
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cde.
ACCESSION AY152052
VERSION AY152052.1 GI:28170842
KEYWORDS
SEGMENT
SOURCE
Dengue virus type 4 (DEN-4)
1 of 4
Dengue virus type 4 (DEN-4)
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ORGANISM Dengue virus type 4
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

REFERENCE 1 (bases 1 to 2552)
 AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndan,V., Gubler,D.J. and McMillan,W.O.
 TITLE Selection-Driven Evolution of Emergent Dengue Virus
 JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
 PUBMED 12832629

REFERENCE 2 (bases 1 to 2552)
 AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndan,V., Gubler,D.J. and McMillan,W.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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ORIGIN

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 Best Local Similarity 89.3%; Pred. No. 0.97;
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Qy 1 CCCATCTCMTCAANNATCCCTGCTGTGG 28
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 DEFINITION Dengue virus type 4 D4.12.1998 polyprotein precursor, gene, partial cds.
 ACCESSION AY152056
 VERSION AY152056.1 GI:28170851
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 SEGMENT Dengue virus type 4 (DEN-4)
 SOURCE Dengue virus type 4
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
 1 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndan,V., Gubler,D.J. and McMillan,W.O.
 TITLE Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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VERSION AY152060.1 GI:28170860
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SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Dengue virus type 4
ORGANISM Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

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DEFINITION
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ACCESSION AY152080
VERSION AY152080.1 GI:28170905
KEYWORDS
SEGMENT
SOURCE
ORGANISM
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
AUTHORS
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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LVLWIGTNSRNTSAMTCIAVGGITLFLGFTVQADMGCVVWSGRELKCGSGLFVVDN
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ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178
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LVLWIGTNSRNTSAMTCIAVGGITLFLGFTVQADMGCVVWSGRELKCGSGLFVVDN
VHTWTEQYKQPESPARLASAILNAHKDVGCGIRSTRLNVNMWKQITNELN"

ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178

RESULT 25
AY152084S1/c AY152084S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS Dengue virus type 4 D4.84_1994 polyprotein precursor, gene, partial
DEFINITION
cds.
ACCESSION AY152084
VERSION AY152084.1 GI:28170914
KEYWORDS
SEGMENT
SOURCE
ORGANISM
i of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
AUTHORS
REFERENCE 2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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glycoprotein"
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/db_xref="GI:28170921"
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TVTYKPLLVAEPEDIDCNLTSTWMTGCTCTQSGERRRKRKSVALTPHSGMGLET
RAETWMSSEGAKHQRVESWILRNPGFALLAGFMAVMIGTGITRTVFFVLMVLAP
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ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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Db 205 CCCATCTCTTCAGAAATCCCTGCTGTTGG 178
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RESULT 26
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LOCUS      2552 bp      RNA      linear      VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.44_1998 polyprotein precursor, gene, partial
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ACCESSION  AY152088
KEYWORDS    AY152088.1  GI:28170923
SEGMENT     1
SOURCE      1
ORGANISM    1 of 4
            Dengue virus type 4 (DEN-4)
            Dengue virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE   1 (bases 1 to 2552)
AUTHORS     Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
            Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
            Selection-Driven Evolution of Emergent Dengue Virus
            Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
            12832629
REFERENCE   2 (bases 1 to 2552)
AUTHORS     Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
            Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
            Direct Submission
            Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
            Piedras, PO Box 23360, San Juan 00931, Puerto Rico
            Location/Qualifiers
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               glycoprotein"
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ORIGIN

Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCCATCTCTCANNATCCCTGCTGTGG 28
DB      205  CCCATCTCTCAGNATCCCTGCTGTGG 178

RESULT 27
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LOCUS      2552 bp      RNA      linear      VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.113_1995VE polyprotein precursor, gene,
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ACCESSION  AY152092
KEYWORDS    AY152092.1  GI:28170932
SEGMENT     1
SOURCE      1
ORGANISM    1 of 4
            Dengue virus type 4 (DEN-4)
            Dengue virus type 4
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Flavivirus; Dengue virus group.
REFERENCE   1 (bases 1 to 2552)
AUTHORS     Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
            Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
            Selection-Driven Evolution of Emergent Dengue Virus
            Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
            12832629
REFERENCE   2 (bases 1 to 2552)
AUTHORS     Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
            Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
            Direct Submission
            Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
            Piedras, PO Box 23360, San Juan 00931, Puerto Rico
            Location/Qualifiers
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AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE        Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL      Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED       12832629
REFERENCE    2 (bases 1 to 2552)
AUTHORS      Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE        Direct Submission
JOURNAL      Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES     source
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LVLWIGTNSRNTSMATCIAGVGITLPLGFTVQADMGCVCVWSGRELKCSGIFVVDN
VHTWTQYKFPESPARLASAILNAHKDGVCGIRSTRLNENVMWKQITNELN"
ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGAACTCCCTGCTGTGG 178

RESULT 29
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LOCUS      Dengue virus type 4 D4.108_1996CR polyprotein precursor, gene,
DEFINITION partial cds.
ACCESSION  AY152104.1 GI:28170959
VERSION     AY152104.1
KEYWORDS    1 of 4
SOURCE      Dengue virus type 4 (DEN-4)
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE      Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL    Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED     12832629
REFERENCE  2 (bases 1 to 2552)
AUTHORS    Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
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Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES     Location/Qualifiers
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VHTWTQYKFPESPARLASAILNAHKDGVCGIRSTRLNENVMWKQITNELN"
ORIGIN
Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
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Db 205 CCCATCTCTTCAGAACTCCCTGCTGTGG 178

RESULT 30
AY152108S1/c AY152108S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS      Dengue virus type 4 D4.3_1987 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION  AY152108
VERSION     AY152108.1 GI:28170968
KEYWORDS    1 of 4
SOURCE      Dengue virus type 4 (DEN-4)
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE      Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL    Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED     12832629
REFERENCE  2 (bases 1 to 2552)
AUTHORS    Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES     Location/Qualifiers
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CCACATCTCTCANNATCCCTGCTCTTGG 28
Db      205  CCACATCTCTTCAGAAATCCCTGCTCTTGG 178

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RESULT 35	
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LOCUS	linear VRL 29-SEP-2003
DEFINITION	Dengue virus type 4 D4.78_1994 polyprotein precursor, gene, partial cds
ACCESSION	AY152128
VERSION	AY152128.1 GI:28171013
KEYWORDS	.
SOURCE	1 of 4
ORGANISM	Dengue virus type 4 (DEN-4)
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
AUTHORS	Bennett S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
TITLE	Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED	12832629
REFERENCE	2 (bases 1 to 2552)
AUTHORS	Bennett S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES	Location/Qualifiers
SOURCE	1..2552

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 VTCAKESCCKIITGNLYQNIENLYVTWTHNGDTHAVGNDTSHNGVTAITTPRSRV
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 HWNYKERMTVFKVPHAKRQDVTVLGSGEGAMHSALAGKATVEDSGDNHMFAGKLCVK
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Query Match      89.3%; Score 25; DB 14; Length 2552;
Best Local Similarity 89.3%; Pred. No. 0.97;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CCGATCTCNCANNATCCCTGCTGTTGG 28
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Db 205 CCATCTCTTCAGAAATCCCTGCTGTGG 178

RESULT 36
 AV15213281/c AV15213281 2552 bp RNA linear VRL 29-SEP-2003
 LOCUS
 DEFINITION Dengue virus type 4 D4.77_1994 polyprotein precursor, gene, partial cds.

ACCESSION AV152132
 VERSION AV152132.1 GI:28171022
 KEYWORDS
 SEGMENTS
 SOURCE
 ORGANISM
 1 of 4
 Dengue virus type 4 (DENV-4)
 Dengue virus type 4
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

REFERENCE
 1 (bases 1 to 2552)
 Bennett S.N., Holmes E.C., Chirivella M., Rodriguez D.M., Beltran M., Vorndam V., Gubler D.J. and McMillan W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

TITLE
 JOURNAL
 PUBMED
 12832629

REFERENCE
 2 (bases 1 to 2552)
 Bennett S.N., Holmes E.C., Chirivella M., Rodriguez D.M., Beltran M., Vorndam V., Gubler D.J. and McMillan W.O. Direct Submission

TITLE
 JOURNAL
 Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES
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CDS

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Query Match 89.3%; Score 25; DB 14; Length 2552;
 Best Local Similarity 89.3%; Pred. No. 0.97;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCTCTTCAGAAATCCCTGCTGTGG 28
 Db 205 CCATCTCTTCAGAAATCCCTGCTGTGG 178

RESULT 37	AV152136S1/c	LOCUS	AV152136S1	2552 bp	RNA	linear	VRL 29-SEP-2003
DEFINITION	Dengue virus type 4	D4.76	1994	polyprotein precursor, gene, partial			


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PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
        Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
        Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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FEATURES
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:03:16 ; Search time 214 Seconds
(without alignments)
774.546 Million cell updates/sec

Title: US-10-085-944-1

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	25	89.3	10616	10 AAD53912	Aad53912 Dengue vi
6	25	89.3	10649	10 AAD53911	Aad53911 Recombina
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C 35	18.8	67.1	2237	13 ADS73977	Ads73977 Skeletal
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C 37	18.8	67.1	5674	2 AAQ32352	Aaq32352 WAGE-1 nu
C 38	18.8	67.1	5674	2 AAQ72477	Aaq72477 Tumour re
C 39	18.8	67.1	5674	2 AAX84113	Aax84113 WAGE-1 ge
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C 44	18.6	66.4	486	4 ABA70225	Aba70225 Human foe
C 45	18.6	66.4	486	4 AAI50355	Aai50355 Probe #19
C 46	18.6	66.4	486	4 AAX44355	Aax44355 Human bon
C 47	18.6	66.4	486	4 AAK18450	Aak18450 Human bra
C 48	18.6	66.4	486	4 ABS44012	Abs44012 Human liv
C 49	18.6	66.4	486	6 ABS18591	Abs18591 Human gen
C 50	18.6	66.4	577	12 ACH80409	Ach80409 Human gen
C 51	18.6	66.4	2300	8 ADA69615	Ada69615 Rice gene
C 52	18.6	66.4	6412	13 ABD33380	Abd33380 Murine ca
C 53	18.6	66.4	61396	13 ABD33379	Abd33379 Murine ca
C 54	18.6	66.4	98634	11 ACN45094	Acn45094 Human gen
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C 57	18.2	65.0	1928	5 ABV30242	Abv30242 Human pro
C 58	18.2	65.0	2385	3 AAZ95009	Aaz95009 Cancer sp
C 59	18.2	65.0	2919	2 AAT51124	Aat51124 Human hom
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98	17.6	62.9	454	12	ADR98583	AdK98583 Human imm	171	17.6	62.9	51365	12	ADM74585	Adm74585 Human car
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103	17.6	62.9	494	4	ABA26083	ABa26083 Probe #45	176	17.4	62.1	345	12	ADP91994	AdP91994 Cotton ex
104	17.6	62.9	494	4	AAK30121	AAK30121 Human bon	177	17.4	62.1	646	9	ACL25103	ACL25103 DNA Clone
105	17.6	62.9	494	4	ABS29768	ABs29768 Human liv	178	17.4	62.1	41637	9	ADA02837	Ada02837 Mouse Map
106	17.6	62.9	494	5	AAI04522	AAi04522 Probe #45	179	17.4	62.1	41637	10	ADB72575	AdB72575 Mouse Map
107	17.6	62.9	494	6	ABSO4703	ABs04703 Human gen	180	17.4	62.1	41637	10	ADC85316	Adc85316 Human MeF
108	17.6	62.9	543	10	AD033396	AdD033396 Mouse mit	181	17.4	62.1	41637	12	ADM74432	AdM74432 Murine ca
109	17.6	62.9	566	4	AAI19205	AAi19205 Probe #91	182	17.4	62.1	88191	8	ABX14763	ABx14763 Genomic D
110	17.6	62.9	566	4	ABA64213	ABa64213 Human foe	c 183	17.2	61.4	255	3	ACAC06226	AcAC06226 Human sec
111	17.6	62.9	566	4	AAK31359	AAK31359 Probe #98	184	17.2	61.4	302	6	ABN25382	ABn25382 Human ORF
112	17.6	62.9	566	4	AAK38411	AAK38411 Human bon	c 185	17.2	61.4	463	6	ABK48587	ABk48587 Human CBF
113	17.6	62.9	566	4	AAK12693	AAK12693 Human bra	186	17.2	61.4	497	4	AAK81891	AAK81891 Human imm
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123	17.6	62.9	966	10	ADH42268	AdH42268 Novel hum	c 196	17.2	61.4	1638	13	ADT46608	AdT46608 Bacterial
124	17.6	62.9	981	12	ADH42260	AdH42260 Novel hum	c 197	17.2	61.4	1822	6	ADG33867	AdG33867 Human sec
125	17.6	62.9	981	12	ADH42266	AdH42266 Novel hum	c 198	17.2	61.4	1927	10	ADG10791	AdG10791 Human STA
126	17.6	62.9	981	12	ADH42262	AdH42262 Novel hum	c 199	17.2	61.4	1927	10	ADG10789	AdG10789 Human STA
127	17.6	62.9	981	12	ADH42264	AdH42264 Novel hum	c 200	17.2	61.4	2277	8	ADA70253	AdA70253 Rice gene
128	17.6	62.9	981	12	ADH42258	AdH42258 Novel hum	c 201	17.2	61.4	4119	4	AAI03912	AAi03912 Human rep
129	17.6	62.9	982	4	AAI9141	AAi9141 Human G-P	c 202	17.2	61.4	4119	5	AAAS40312	AAa40312 DNA encod
130	17.6	62.9	1064	2	RAAX90349	RAaX90349 Human CD2	c 203	17.2	61.4	4119	11	ADJ09518	AdJ09518 Human pro
131	17.6	62.9	1092	5	ADL63111	AdL63111 Human ova	c 204	17.2	61.4	4124	4	AAI03911	AAi03911 Human rep
132	17.6	62.9	1151	4	AAD19140	AAI19140 Human G-P	c 205	17.2	61.4	4124	5	AAAS40311	AAa40311 DNA encod
133	17.6	62.9	1151	12	ADH42256	AdH42256 Novel hum	c 206	17.2	61.4	4124	11	ADJ09517	AdJ09517 Human pro
134	17.6	62.9	1345	10	ADC86302	Adc86302 Human GPC	c 207	17.2	61.4	5410	3	AAK83706	AAK83706 Human lam
135	17.6	62.9	1400	5	AAAS42251	AAa42251 Human CDN	c 208	17.2	61.4	5498	3	AAK83705	AAK83705 Human lam
136	17.6	62.9	1400	6	ABK37537	ABk37537 DNA encod	c 209	17.2	61.4	5781	10	ADC01876	Adc01876 Human DNA
137	17.6	62.9	1514	2	AAQ21167	AAQ21167 Human CD2	c 210	17.2	61.4	5781	10	ADC01878	Adc01878 Human DNA
138	17.6	62.9	1514	2	AAAT36257	AAaT36257 Human CD2	c 211	17.2	61.4	5942	3	AAK83704	AAK83704 Human lam
139	17.6	62.9	1514	2	AAAT14707	AAaT14707 Human CD2	c 212	17.2	61.4	6204	3	AAK83703	AAK83703 Human lam
140	17.6	62.9	1514	2	AAV63445	AAv63445 Human CD2	c 213	17.2	61.4	6204	6	ABN96539	ABn96539 Gene #303
141	17.6	62.9	1514	2	AAV81203	AAV81203 Human CD2	c 214	17.2	61.4	6204	13	ADR87599	AdR87599 Human lam
142	17.6	62.9	1514	3	AAAS0581	AAaS0581 Human cel	c 215	17.2	61.4	6297	12	ADP08395	AdP08395 Human lam
143	17.6	62.9	1514	3	AAZ29325	AAz29325 Human CD2	c 216	17.2	61.4	6482	6	ABQ93499	ABq93499 Human CDN
144	17.6	62.9	1514	4	AAAS0175	AAaS0175 Human lym	c 217	17.2	61.4	6752	10	ADJ56228	AdJ56228 Human CDN
145	17.6	62.9	1514	6	ABA99035	ABa99035 Human CD2	c 218	17.2	61.4	6754	6	ABZ35423	ABz35423 Human gen
146	17.6	62.9	1514	10	ADD25537	AdD25537 Binding d	c 219	17.2	61.4	14002	10	ADC87691	Adc87691 Human mam
147	17.6	62.9	1514	11	ADJ31990	AdJ31990 Human CDN	c 220	17.2	61.4	19868	12	ADP20457	AdP20457 Human tra
148	17.6	62.9	1514	12	ADO49343	AdO49343 Human CD2	c 221	17.2	61.4	20001	13	ACN37214	AcN37214 Human per
149	17.6	62.9	1574	1	AAAN90607	AAaN90607 CD28 anti	c 222	17.2	61.4	23587	4	AAAL07100	AAaL07100 Human rep
150	17.6	62.9	1868	5	ABA20104	ABa20104 Human ner	c 223	17.2	61.4	42016	13	ABD32962	ABd32962 Human can
151	17.6	62.9	2105	12	ADO58117	AdO58117 Influenza	c 224	17.2	61.4	51474	5	AAF97846	AAf97846 Human neu
152	17.6	62.9	2170	3	AAFL6207	AAfL6207 Human pro	c 225	17.2	61.4	57296	4	AAK78847	AAK78847 Human imm
153	17.6	62.9	2238	2	AAAT06476	AAaT06476 Bovine ca	c 226	17.2	61.4	57296	4	AAK78170	AAK78170 Human imm
154	17.6	62.9	2567	4	AAHL18261	AAHl18261 Human CDN	c 227	17.2	61.4	57296	4	AAK79364	AAK79364 Human imm
155	17.6	62.9	3803	6	AAAL49546	AAaL49546 Human CD2	c 228	17.2	61.4	57296	4	AAK86799	AAK86799 Human imm
156	17.6	62.9	3804	8	ABV75351	ABv75351 Human CD2	c 229	17.2	61.4	59393	10	ADC85449	Adc85449 Mouse Git
157	17.6	62.9	3804	9	ADA02991	AdA02991 Human CD2	c 230	17.2	61.4	59394	9	ADA02969	AdA02969 Mouse Git
158	17.6	62.9	3804	10	ADB72729	ABd72729 Human CD2	c 231	17.2	61.4	59394	10	ADB72707	ABd72707 Mouse Git
159	17.6	62.9	3804	10	ADC85471	Adc85471 Human CD2	c 232	17.2	61.4	59394	12	ADM74564	AdM74564 Murine ca
160	17.6	62.9	3804	12	ADM74586	AdM74586 Human car	c 233	17.2	61.4	95400	12	ADP08388	AdP08388 Human lam
161	17.6	62.9	3804	12	ADN05855	AdN05855 Antipsori	c 234	17.2	61.4	110000	11	ACN44150	AcN44150 3 of
162	17.6	62.9	3806	6	AAD21976	AAaD21976 Human CD2	c 235	17.2	61.4	160921	11	ACN44962	AcN44962 Human gen
163	17.6	62.9	4723	5	AAAS87860	AAaS87860 DNA encod	c 236	17.2	61.4	171936	6	ABSS5655	ABsS5655 Human SUL
164	17.6	62.9	19025	6	AAAL48838	AAaL48838 Human pro	c 237	17.2	61.4	171936	12	ADN16205	AdN16205 Mouse sul
165	17.6	62.9	22622	4	ABL28510	ABl28510 Drosophi	c 238	17.2	61.4	220756	12	ADG86300	AdG86300 Human SMR
166	17.6	62.9	31960	9	ACD18998	ACd18998 E. coli 0	c 239	17.2	61.4	233380	11	ACN44282	AcN44282 Human gen

240	17-2	61.4	338702	11	ACN44042	Acn44042 Human gen	313	17	60.7	4275	1	AAN80446	Aan80446 Modified
c 241	17	60.7	121	4	ABA79007	Aba79007 Factor VI	314	17	60.7	4275	1	AAN80654	Aan80654 DNA encod
242	17	60.7	121	4	ABA79010	Aba79010 Factor VI	315	17	60.7	4371	11	ADM98123	Adm98123 Human fac
c 243	17	60.7	121	4	ABA79031	Aba79031 Factor VI	316	17	60.7	4545	1	AAN80444	Aan80444 Modified
244	17	60.7	121	4	ABA79018	Aba79018 Factor VI	317	17	60.7	4616	1	AAN81545	Aan81545 Human fac
c 245	17	60.7	121	4	ABA79023	Aba79023 Factor VI	318	17	60.7	4629	6	ABX88293	Abx88293 Human fac
c 246	17	60.7	121	4	ABA78999	Aba78999 Factor VI	319	17	60.7	4629	6	ABN84384	Abn84384 Human B d
247	17	60.7	121	4	ABA79002	Aba79002 Factor VI	320	17	60.7	4670	2	AAV23339	AAv23339 Human fac
c 248	17	60.7	121	4	ABA79011	Aba79011 Factor VI	321	17	60.7	4830	1	AAN81544	Aan81544 Human fac
249	17	60.7	121	4	ABA79030	Aba79030 Factor VI	322	17	60.7	4832	2	AAV19581	AAv19581 Human fac
c 250	17	60.7	121	4	ABA79015	Aba79015 Factor VI	323	17	60.7	4832	2	AAV15338	AAv15338 Human fac
c 251	17	60.7	121	4	ABA78998	Aba78998 Factor VI	324	17	60.7	4939	3	AAV15338	AAv15338 Human fac
252	17	60.7	121	4	ABA79006	Aba79006 Factor VI	325	17	60.7	4999	4	AAV15338	AAv15338 Human fac
c 253	17	60.7	121	4	ABA79006	Aba79006 Factor VI	325	17	60.7	4999	4	AAV15338	AAv15338 Human fac
c 254	17	60.7	121	4	ABA79026	Aba79026 Factor VI	326	17	60.7	5035	2	AAV15338	AAv15338 Human fac
255	17	60.7	121	4	ABA79032	Aba79032 Factor VI	327	17	60.7	5035	2	AAV15338	AAv15338 Human fac
c 256	17	60.7	121	4	ABA79014	Aba79014 Factor VI	328	17	60.7	6242	12	ADO44189	Ado44189 Factor VI
c 257	17	60.7	121	4	ABA79019	Aba79019 Factor VI	329	17	60.7	6300	2	AAV15338	AAv15338 Human fac
c 258	17	60.7	121	4	ABA79027	Aba79027 Factor VI	330	17	60.7	6300	2	AAV15338	AAv15338 Human fac
259	17	60.7	201	13	ADQ44445	Adq44445 Myocardia	331	17	60.7	6996	4	ADL18171	Adl18171 Human mat
260	17	60.7	201	13	ADQ44450	Adq44450 Myocardia	332	17	60.7	6996	11	ADM98118	Adm98118 Human fac
261	17	60.7	201	13	ADQ44972	Adq44972 Myocardia	333	17	60.7	6999	10	ABV99883	Abv99883 Human fac
262	17	60.7	201	13	ADQ44571	Adq44571 Myocardia	334	17	60.7	7053	2	AAV15338	AAv15338 Human fac
263	17	60.7	201	13	ADQ44590	Adq44590 Myocardia	335	17	60.7	7056	2	AAV15338	AAv15338 Human fac
264	17	60.7	201	13	ADQ44922	Adq44922 Myocardia	336	17	60.7	7059	1	AAN81543	Aan81543 Human fac
265	17	60.7	201	13	ADQ44578	Adq44578 Myocardia	337	17	60.7	7190	13	ACN43250	Acn43250 Human dia
266	17	60.7	201	13	ADQ44584	Adq44584 Myocardia	338	17	60.7	7440	1	AAN50375	Aan50375 DNA seque
267	17	60.7	201	13	ADQ44573	Adq44573 Myocardia	339	17	60.7	7440	1	AAN50375	Aan50375 DNA seque
268	17	60.7	201	13	ADQ44922	Adq44922 Myocardia	340	17	60.7	7931	10	ACC78883	Acc78883 Human fac
269	17	60.7	201	13	ADQ44591	Adq44591 Myocardia	341	17	60.7	7931	12	ADN49701	Adn49701 Human fac
270	17	60.7	201	13	ADQ44974	Adq44974 Myocardia	342	17	60.7	7944	4	AAF84647	Aaf84647 Plasmid D
271	17	60.7	201	13	ADQ44979	Adq44979 Myocardia	343	17	60.7	7983	4	AAK73139	Aak73139 Human imm
272	17	60.7	201	13	ADQ44985	Adq44985 Myocardia	344	17	60.7	8241	1	AAN81439	Aan81439 Factor VI
273	17	60.7	201	13	ADQ44593	Adq44593 Myocardia	345	17	60.7	8241	1	AAN81096	Aan81096 cDNA sequ
274	17	60.7	201	13	ADQ44845	Adq44845 Myocardia	346	17	60.7	8720	4	ADL18172	Adl18172 Human fac
275	17	60.7	201	13	ADQ44846	Adq44846 Myocardia	347	17	60.7	8967	2	AAV23339	AAv23339 Factor VI
276	17	60.7	201	13	ADQ44980	Adq44980 Myocardia	348	17	60.7	8967	5	AAV23339	AAv23339 Factor VI
277	17	60.7	201	13	ADQ44994	Adq44994 Myocardia	349	17	60.7	8967	6	AAV23339	AAv23339 Factor VI
278	17	60.7	201	13	ADQ44521	Adq44521 Myocardia	350	17	60.7	8975	1	AAN50054	Aan50054 Human fac
279	17	60.7	201	13	ADQ44978	Adq44978 Myocardia	351	17	60.7	8975	3	AAZ38604	Aaz38604 Human ful
280	17	60.7	201	13	ADQ44991	Adq44991 Myocardia	352	17	60.7	9009	2	AAQ50185	Aaq50185 Human fac
281	17	60.7	201	13	ADQ44551	Adq44551 Myocardia	353	17	60.7	9009	2	AAV61548	AAv61548 Factor VI
282	17	60.7	201	13	ADQ44579	Adq44579 Myocardia	354	17	60.7	9009	2	AAV12112	AAv12112 Homo sapi
283	17	60.7	201	13	ADQ44952	Adq44952 Myocardia	355	17	60.7	9009	2	AAV25810	AAv25810 Human fac
284	17	60.7	201	13	ADQ44977	Adq44977 Myocardia	356	17	60.7	9009	2	AAV18884	AAv18884 Homo sapi
285	17	60.7	201	13	ADQ44576	Adq44576 Myocardia	357	17	60.7	9009	2	AAV18884	AAv18884 Homo sapi
286	17	60.7	201	13	ADQ44577	Adq44577 Myocardia	358	17	60.7	9009	2	AAV18884	AAv18884 Homo sapi
287	17	60.7	201	13	ADQ44444	Adq44444 Myocardia	359	17	60.7	9009	5	AAV18884	AAv18884 Homo sapi
288	17	60.7	201	13	ADQ44851	Adq44851 Myocardia	360	17	60.7	9009	5	AAV18884	AAv18884 Homo sapi
289	17	60.7	306	6	ABQ73837	Abq73837 Human col	361	17	60.7	9009	10	ADK48887	Adk48887 wild type
c 290	17	60.7	377	5	AAH93969	Aah93969 Human col	362	17	60.7	9009	11	ADM98116	Adm98116 Human fac
c 291	17	60.7	405	6	ABN78101	Abn78101 Human ORF	363	17	60.7	9009	12	ADF09121	Adf09121 Human fac
c 292	17	60.7	494	6	ABQ73838	Abq73838 Human col	364	17	60.7	9029	4	AAV60309	AAv60309 Human fac
c 293	17	60.7	497	10	ADH81719	Adh81719 Arabidops	365	17	60.7	9029	8	ABV77052	Abv77052 Nucleotid
c 294	17	60.7	504	12	ACH75253	Ach75253 Human gen	366	17	60.7	9068	2	AAV15359	AAv15359 Human fac
c 295	17	60.7	524	12	ACH73493	Ach73493 Human gen	367	17	60.7	9068	2	AAV15359	AAv15359 Human fac
c 296	17	60.7	558	5	AAH94381	Aah94381 Human fo	368	17	60.7	9068	2	AAV15359	AAv15359 Human fac
c 297	17	60.7	566	4	AAI19355	Aai19355 Probe #92	369	17	60.7	9164	2	AAV15359	AAv15359 Human fac
c 298	17	60.7	807	13	ADN46977	Adn46977 Bacterial	370	17	60.7	9220	13	AAV15359	AAv15359 Human fac
c 299	17	60.7	927	8	ADA70754	Ada70754 Rice gene	371	17	60.7	9354	2	AAV15359	AAv15359 Human fac
c 300	17	60.7	1422	8	ABX08491	Abx08491 DNA encod	372	17	60.7	10698	4	AAV15359	AAv15359 Human fac
c 301	17	60.7	1489	4	ABL06283	AbL06283 Drosophi	373	17	60.7	10698	4	AAV15359	AAv15359 Human fac
c 302	17	60.7	1867	12	ADL12902	Adl12902 Human ste	374	17	60.7	10698	4	AAV15359	AAv15359 Human fac
c 303	17	60.7	2000	12	ADJ41159	Adj41159 Plant cDN	375	17	60.7	11846	2	AAV15359	AAv15359 Human fac
c 304	17	60.7	2283	3	ADP20776	Adp20776 Factor VI	376	17	60.7	11933	3	AAV15359	AAv15359 Human fac
c 305	17	60.7	2285	6	ADE64591	Ade64591 Recombina	377	17	60.7	11933	3	AAV15359	AAv15359 Human fac
c 306	17	60.7	2348	8	ACC46288	Acc46288 Human dit	378	17	60.7	12022	2	AAV15359	AAv15359 Human fac
c 307	17	60.7	2446	4	ABL13927	AbL13927 Drosophi	379	17	60.7	12022	2	AAV15359	AAv15359 Human fac
c 308	17	60.7	3268	3	AAC76087	Aac76087 Human ORF	380	17	60.7	12394	4	AAV15359	AAv15359 Human fac
c 309	17	60.7	3391	4	ABL22324	AbL22324 Drosophi	381	17	60.7	12445	3	AAV15359	AAv15359 Human fac
c 310	17	60.7	3714	4	ABL06282	AbL06282 Drosophi	382	17	60.7	12445	3	AAV15359	AAv15359 Human fac
c 311	17	60.7	3988	4	ABL13226	AbL13226 Drosophi	383	17	60.7	12445	3	AAV15359	AAv15359 Human fac
c 312	17	60.7	4272	1	AAN80447	Aan80447 Modified	384	17	60.7	12445	3	AAV15359	AAv15359 Human fac

c 386	17	60.7	42325	10	ADB74382	Adb74382	Mycobacte
c 387	17	60.7	45783	12	ADQ97255	Adq97255	Human can
c 388	17	60.7	55998	9	ADA02975	Ada02975	Mouse Anp
c 389	17	60.7	55998	10	ADB72713	Adb72713	Mouse Anp
c 390	17	60.7	55998	10	ADC85455	Adc85455	Mouse Anp
c 391	17	60.7	55998	12	ADM74570	Adm74570	Murine ca
c 392	17	60.7	110000	6	ABA03041_06		
c 393	17	60.7	110000	6	ABA03041_07		
c 394	17	60.7	110000	9	ADAI3411_1		
c 395	17	60.7	110000	12	ADQ59446_1		
c 396	17	60.7	111084	12	ADQ18808	Adq18808	Human sof
c 397	17	60.7	135462	12	ADQ97081	Adq97081	Mouse can
c 398	17	60.7	140152	12	ADP03002	Adp03002	Human hou
c 399	17	60.7	140152	13	ADS8500	Ads8500	Human hou
c 400	17	60.7	154394	12	ADQ17784	Adq17784	Human sof
c 401	17	60.7	181684	11	ACN44374	Acn44374	Human gen
c 402	17	60.7	209484	11	ACN44126	Acn44126	Human gen
c 403	16.8	60.0	222	3	AAC23557	Aac23557	Human sec
c 404	16.8	60.0	246	10	ABZ40682	Abz40682	N. gonorr
c 405	16.8	60.0	297	6	ABL73285	Ab173285	Corn tass
c 406	16.8	60.0	437	4	RAK89251	Rak89251	Human dig
c 407	16.8	60.0	437	4	RAK89249	Rak89249	Human dig
c 408	16.8	60.0	437	4	AA105890	Aal05890	Human rep
c 409	16.8	60.0	437	4	AA105892	Aal05892	Human rep
c 410	16.8	60.0	437	4	ABL98456	Ab198456	Human tes
c 411	16.8	60.0	437	4	ABL98454	Ab198454	Human tes
c 412	16.8	60.0	437	8	ABZ74630	Abz74630	Secreted
c 413	16.8	60.0	437	8	ABZ74632	Abz74632	Secreted
c 414	16.8	60.0	437	10	ABZ68152	Abz68152	Human sec
c 415	16.8	60.0	437	10	ABZ68150	Abz68150	Human sec
c 416	16.8	60.0	448	12	ADP63664	Adp63664	Maize car
c 417	16.8	60.0	498	6	ABN70549	Abn70549	Streptoco
c 418	16.8	60.0	562	4	AAH09672	Aah09672	Human cdn
c 419	16.8	60.0	981	10	ADF01883	Adf01883	Bacterial
c 420	16.8	60.0	1617	4	AAH17224	Aah17224	Human cdn
c 421	16.8	60.0	5148	12	ADQ64442	Adq64442	Novel hum
c 422	16.8	60.0	8464	3	AAZ88665	Aaz88665	Murine NI
c 423	16.8	60.0	9480	12	ADK13933	Adk13933	Mouse met
c 424	16.8	60.0	10087	12	ADK13927	Adk13927	Mouse met
c 425	16.8	60.0	19951	8	ABZ24596	Abz24596	Human ova
c 426	16.8	60.0	19951	10	ADJ63173	Adj63173	Human nuc
c 427	16.8	60.0	49634	6	ABL68647	Ab168647	Kidney ca
c 428	16.8	60.0	102634	3	AAA81464	Aaa81464	N. mening
c 429	16.8	60.0	110000	3	AAA81490_10		
c 430	16.8	60.0	110000	6	ABN71527_16		
c 431	16.8	60.0	144792	10	ADC87620	Adc87620	Human GPC
c 432	16.8	60.0	186528	10	ADL13638	Adl13638	Osteoarth
c 433	16.8	60.0	349881	10	ADC86642	Adc86642	Human GPC
c 434	16.8	60.0	349880	3	AAE21609	Aae21609	Neisseria
c 435	16.6	59.3	138	12	ACH88771	Ach88771	Human gen
c 436	16.6	59.3	201	13	ADQ44951	Adq44951	Myocardia
c 437	16.6	59.3	201	13	ADQ44446	Adq44446	Myocardia
c 438	16.6	59.3	201	13	ADQ44847	Adq44847	Myocardia
c 439	16.6	59.3	201	13	ADQ44550	Adq44550	Myocardia
c 440	16.6	59.3	222	2	AA109809	Aat09809	Tomato ge
c 441	16.6	59.3	271	6	ABN77190	Abn77190	Human ORF
c 442	16.6	59.3	324	2	AA186287	Aat86287	Coding se
c 443	16.6	59.3	393	4	AA185826	Aai85826	Human pol
c 444	16.6	59.3	394	3	AAC03613	Aac03613	Human sec
c 445	16.6	59.3	413	6	ABN79122	Abn79122	Human ATP
c 446	16.6	59.3	462	9	ACH13136	Ach13136	Human adu
c 447	16.6	59.3	474	4	AA111933	Aai11933	Probe #18
c 448	16.6	59.3	474	4	ABA53641	Aba53641	Human foe
c 449	16.6	59.3	474	4	AA133265	Aai33265	Probe #19
c 450	16.6	59.3	474	4	ABA43213	Aba43213	Human bre
c 451	16.6	59.3	474	4	ABA23394	Aba23394	Probe #18
c 452	16.6	59.3	474	4	AAK27361	Aak27361	Human bon
c 453	16.6	59.3	474	4	AAK01904	Aak01904	Human bra
c 454	16.6	59.3	474	4	ABS26930	Abs26930	Human liv
c 455	16.6	59.3	474	5	AA101870	Aai01870	Probe #18
c 456	16.6	59.3	474	6	ABS01872	Abs01872	Human gen
c 457	16.6	59.3	488	9	ACL19994	Acl19994	DNA clone
c 458	16.6	59.3	500	4	ABA46485	Aba46485	Human bre
c 386	17	60.7	42325	10	ADB74382	Adb74382	Mycobacte
c 387	17	60.7	45783	12	ADQ97255	Adq97255	Human can
c 388	17	60.7	55998	9	ADA02975	Ada02975	Mouse Anp
c 389	17	60.7	55998	10	ADB72713	Adb72713	Mouse Anp
c 390	17	60.7	55998	10	ADC85455	Adc85455	Mouse Anp
c 391	17	60.7	55998	12	ADM74570	Adm74570	Murine ca
c 392	17	60.7	110000	6	ABA03041_06		
c 393	17	60.7	110000	6	ABA03041_07		
c 394	17	60.7	110000	9	ADAI3411_1		
c 395	17	60.7	110000	12	ADQ59446_1		
c 396	17	60.7	111084	12	ADQ18808	Adq18808	Human sof
c 397	17	60.7	135462	12	ADQ97081	Adq97081	Mouse can
c 398	17	60.7	140152	12	ADP03002	Adp03002	Human hou
c 399	17	60.7	140152	13	ADS8500	Ads8500	Human hou
c 400	17	60.7	154394	12	ADQ17784	Adq17784	Human sof
c 401	17	60.7	181684	11	ACN44374	Acn44374	Human gen
c 402	17	60.7	209484	11	ACN44126	Acn44126	Human gen
c 403	16.8	60.0	222	3	AAC23557	Aac23557	Human sec
c 404	16.8	60.0	246	10	ABZ40682	Abz40682	N. gonorr
c 405	16.8	60.0	297	6	ABL73285	Ab173285	Corn tass
c 406	16.8	60.0	437	4	RAK89251	Rak89251	Human dig
c 407	16.8	60.0	437	4	RAK89249	Rak89249	Human dig
c 408	16.8	60.0	437	4	AA105890	Aal05890	Human rep
c 409	16.8	60.0	437	4	AA105892	Aal05892	Human rep
c 410	16.8	60.0	437	4	ABL98456	Ab198456	Human tes
c 411	16.8	60.0	437	4	ABL98454	Ab198454	Human tes
c 412	16.8	60.0	437	8	ABZ74630	Abz74630	Secreted
c 413	16.8	60.0	437	8	ABZ74632	Abz74632	Secreted
c 414	16.8	60.0	437	10	ABZ68152	Abz68152	Human sec
c 415	16.8	60.0	437	10	ABZ68150	Abz68150	Human sec
c 416	16.8	60.0	448	12	ADP63664	Adp63664	Maize car
c 417	16.8	60.0	498	6	ABN70549	Abn70549	Streptoco
c 418	16.8	60.0	562	4	AAH09672	Aah09672	Human cdn
c 419	16.8	60.0	981	10	ADF01883	Adf01883	Bacterial
c 420	16.8	60.0	1617	4	AAH17224	Aah17224	Human cdn
c 421	16.8	60.0	5148	12	ADQ64442	Adq64442	Novel hum
c 422	16.8	60.0	8464	3	AAZ88665	Aaz88665	Murine NI
c 423	16.8	60.0	9480	12	ADK13933	Adk13933	Mouse met
c 424	16.8	60.0	10087	12	ADK13927	Adk13927	Mouse met
c 425	16.8	60.0	19951	8	ABZ24596	Abz24596	Human ova
c 426	16.8	60.0	19951	10	ADJ63173	Adj63173	Human nuc
c 427	16.8	60.0	49634	6	ABL68647	Ab168647	Kidney ca
c 428	16.8	60.0	102634	3	AAA81464	Aaa81464	N. mening
c 429	16.8	60.0	110000	3	AAA81490_10		
c 430	16.8	60.0	110000	6	ABN71527_16		
c 431	16.8	60.0	144792	10	ADC87620	Adc87620	Human GPC
c 432	16.8	60.0	186528	10	ADL13638	Adl13638	Osteoarth
c 433	16.8	60.0	349881	10	ADC86642	Adc86642	Human GPC
c 434	16.8	60.0	349880	3	AAE21609	Aae21609	Neisseria
c 435	16.6	59.3	138	12	ACH88771	Ach88771	Human gen
c 436	16.6	59.3	201	13	ADQ44951	Adq44951	Myocardia
c 437	16.6	59.3	201	13	ADQ44446	Adq44446	Myocardia
c 438	16.6	59.3	201	13	ADQ44847	Adq44847	Myocardia
c 439	16.6	59.3	201	13	ADQ44550	Adq44550	Myocardia
c 440	16.6	59.3	222	2	AA109809	Aat09809	Tomato ge
c 441	16.6	59.3	271	6	ABN77190	Abn77190	Human ORF
c 442	16.6	59.3	324	2	AA186287	Aat86287	Coding se
c 443	16.6	59.3	393	4	AA185826	Aai85826	Human pol
c 444	16.6	59.3	394	3	AAC03613	Aac03613	Human sec
c 445	16.6	59.3	413	6	ABN79122	Abn79122	Human ATP
c 446	16.6	59.3	462	9	ACH13136	Ach13136	Human adu
c 447	16.6	59.3	474	4	AA111933	Aai11933	Probe #18
c 448	16.6	59.3	474	4	ABA53641	Aba53641	Human foe
c 449	16.6	59.3	474	4	AA133265	Aai33265	Probe #19
c 450	16.6	59.3	474	4	ABA43213	Aba43213	Human bre
c 451	16.6	59.3	474	4	ABA23394	Aba23394	Probe #18
c 452	16.6	59.3	474	4	AAK27361	Aak27361	Human bon
c 453	16.6	59.3	474	4	AAK01904	Aak01904	Human bra
c 454	16.6	59.3	474	4	ABS26930	Abs26930	Human liv
c 455	16.6	59.3	474	5	AA101870	Aai01870	Probe #18
c 456	16.6	59.3	474	6	ABS01872	Abs01872	Human gen
c 457	16.6	59.3	488	9	ACL19994	Acl19994	DNA clone
c 458	16.6	59.3	500	4	ABA46485	Aba46485	Human bre
c 386	17	60.7	42325	10	ADB74382	Adb74382	Mycobacte
c 387	17	60.7	45783	12	ADQ97255	Adq97255	Human can
c 388	17	60.7	55998	9	ADA02975	Ada02975	Mouse Anp
c 389	17	60.7	55998	10	ADB72713	Adb72713	Mouse Anp
c 390	17	60.7	55998	10	ADC85455	Adc85455	Mouse Anp
c 391	17	60.7	55998	12	ADM74570	Adm74570	Murine ca
c 392	17	60.7	110000	6	ABA03041_06		
c 393	17	60.7	110000	6	ABA03041_07		
c 394	17	60.7	110000	9	ADAI3411_1		
c 395	17	60.7	110000	12	ADQ59446_1		
c 396	17	60.7	111084	12	ADQ18808	Adq18808	Human sof
c 397	17	60.7	135462	12	ADQ97081	Adq97081	Mouse can
c 398	17	60.7	140152	12	ADP03002	Adp03002	Human hou
c 399	17	60.7	140152	13	ADS8500	Ads8500	Human hou
c 400	17	60.7	154394	12	ADQ17784	Adq17784	Human sof
c 401	17	60.7	181684	11	ACN44374	Acn44374	Human gen
c 402	17	60.7	209484	11	ACN44126	Acn44126	Human gen
c 403	16.8	60.0					


```
DR WPI; 2003-066244/06.
XX
XX New pharmaceutical compositions containing dengue nucleic acids, useful
PT as a vaccine, particularly for inducing a protective immune response in
PT mammalian subjects against the dengue virus infection.
XX
XX Disclosure; Col 17-20; 26pp; English.
XX
XX The invention discloses a pharmaceutical composition capable of inducing
CC an immune response in a mammalian subject, comprising an immunogenic
CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
CC which includes the envelope and membrane (Brem) genes of a dengue type 1,
CC 2, 3, or 4 virus. Dengue virus (DENV) belongs to the flavivirus genus of
CC the family Flaviviridae and is a positive strand RNA virus encoding ten
CC proteins. These genes are translated as a polypeptide which is cleaved by
CC host and viral proteinases. The virus envelope protein is a major antigen
CC which can be targeted by neutralising antibodies. The membrane protein
CC also appears on the virion surface and is required for proper processing
CC of the envelope protein. Dengue viruses are transmitted primarily by the
CC mosquito, Aedes aegypti, and can lead to human illnesses ranging from
CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
CC dengue shock syndrome (DSS). Secondary infections, with a different
CC serotype, may lead to an immune enhancement phenomenon. The compositions
CC of the invention are DNA vaccines which are injected into the animal as a
CC technique of gene therapy. The composition is useful as a vaccine,
CC particularly for inducing a protective immune response in mammalian
CC subjects against the dengue virus infection. The sequence presented is
CC the dengue virus type 2 (DENV2) structural gene genome segment
XX
XX Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;
SQ
Query Match 89.3%; Score 25; DB 8; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.4;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTTCAGTACCCCTGCTGTGG 28
Db 228 CCCATCTCTTCAGTACCCCTGCTGTGG 201
RESULT 4
ADG93319/c
ID ADG93319 standard; DNA; 2423 BP.
XX
XX ADG93319;
XX
XX 11-MAR-2004 (first entry)
XX
XX DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.
XX immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
XX dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
XX dengue virus; delta30; attenuating mutation; humoral response;
XX cellular response; non-structural protein; structural protein;
XX dengue virus serotype; gene; ds; plasmid P2.
XX
XX Dengue virus type 1.
XX
XX WO2003092592-A2.
XX
XX 13-NOV-2003.
XX
XX 25-APR-2003; 2003WO-US013279.
XX
XX 03-MAY-2002; 2002US-0377860P.
XX 23-DEC-2002; 2002US-0436500P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX Hanley K;
XX
XX WPI; 2004-022612/02.
XX
DR
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P-PSDB; ADG93320.
XX
XX New tetravalent vaccine containing a common nucleotide deletion in the 3'
PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
XX
XX Disclosure; SEQ ID NO 52; 181pp; English.
XX
XX This invention relates to a novel immunogenic composition being
CC tetravalent and containing a common nucleotide deletion in the 3'
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN1 ME chimeric region DNA which is related to
CC the invention.
XX
XX Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;
SQ
Query Match 89.1%; Score 25; DB 12; Length 2423;
Best Local Similarity 89.3%; Pred. No. 0.41;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCCATCTCTTCAGTACCCCTGCTGTGG 28
Db 306 CCCATCTCTTCAGTACCCCTGCTGTGG 279
RESULT 5
AAD53912/c
ID AAD53912 standard; DNA; 10616 BP.
XX
XX AAD53912;
XX
XX 28-MAY-2003 (first entry)
XX
XX Dengue virus type 2 strain rDEN2/4delta30 DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX Dengue virus.
XX
XX Location/Qualifiers
XX Key 97..10263
XX CDS /tag= a
XX /product= "DEN4 strain rDEN2/4delta30 protein"
XX mat_peptide 97..438
XX /tag= c
XX /product= "Anchored capsid protein"
XX mat_peptide 97..396
XX /tag= b
XX /product= "Virion capsid protein"
XX mat_peptide 439..936
XX /tag= d
XX /product= "Membrane precursor protein"
XX mat_peptide 712..936
XX /tag= e
XX /product= "Membrane protein"
XX mat_peptide 937..2421
XX /tag= f
XX /product= "Envelope protein"
XX mat_peptide 2422..3477
XX /tag= g
XX /product= "NS1 protein"
XX mat_peptide 3478..4131
```

```

FT FT      /*tag= h
FT FT      /product= "NS2A protein"
FT FT      4132.4521
FT FT      /*tag= i
FT FT      /product= "NS2B protein"
FT FT      4522.6375
FT FT      /*tag= j
FT FT      /product= "NS3 protein"
FT FT      6376.6756
FT FT      /*tag= k
FT FT      /product= "NS4A protein"
FT FT      6757.6825
FT FT      /*tag= l
FT FT      /product= "2K protein"
FT FT      6826.7560
FT FT      /*tag= m
FT FT      /product= "NS4B protein"
FT FT      7561.10260
FT FT      /*tag= n
FT FT      /product= "NS5 protein"
XX
XX WO200295075-A1.
PN
XX
XX
XX 28-NOV-2002.
PD
XX
XX 22-MAY-2002; 2002WO-US016308.
PF
XX
XX 22-MAY-2001; 2001US-0293049P.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX
XX P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain
XX rDEN2/4delta30 DNA
XX
XX Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
XX
XX Query Match      89.3%; Score 25; DB 10; Length 10616;
XX Best Local Similarity 89.3%; Pred. No. 0.52;
XX Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX Qy      1 CCCATCTCTCANNATCCCTGCTGTGG 28
XX      |||||
XX Db      304 CCCATCTCTTCAGTATCCCTGCTGTGG 277
XX
XX RESULT 6
XX AAD53911/c
XX ID AAD53911 standard; DNA; 10649 BP.
XX
XX AC AAD53911;
XX
XX DT 28-MAY-2003 (first entry)
XX
DE Recombinant dengue virus type 4 strain rDEN4 DNA.
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
XX
XX Dengue virus.
XX
XX Key Location/Qualifiers
XX CDS 102..10649
XX
XX FT      /*tag= a
XX FT      /product= "DEN4 strain rDEN4 protein"
XX FT      102..440
XX FT      /*tag= c
XX FT      /product= "Anchored capsid protein"
XX FT      102..398
XX FT      /*tag= b
XX FT      /product= "Virion capsid protein"
XX FT      441..938
XX FT      /*tag= d
XX FT      /product= "Membrane precursor protein"
XX FT      714..938
XX FT      /*tag= e
XX FT      /product= "Membrane protein"
XX FT      939..2423
XX FT      /*tag= f
XX FT      /product= "Envelope protein"
XX FT      2424..3479
XX FT      /*tag= g
XX FT      /product= "NS1 protein"
XX FT      3480..4133
XX FT      /*tag= h
XX FT      /product= "NS2A protein"
XX FT      4134..4523
XX FT      /*tag= i
XX FT      /product= "NS2B protein"
XX FT      4524..6377
XX FT      /*tag= j
XX FT      /product= "NS3 protein"
XX FT      6378..6758
XX FT      /*tag= k
XX FT      /product= "NS4A protein"
XX FT      6638..7562
XX FT      /*tag= m
XX FT      /product= "NS4B protein"
XX FT      6759..6827
XX FT      /*tag= l
XX FT      /product= "2K protein"
XX FT      7563..10262
XX FT      /*tag= n
XX FT      /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
XX
XX P-PSDB; AAE35313.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 131-132; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a

```


CC phenotype in which the viral genome is modified by introduction of a
CC mutation, singly or in combination, taken from mutations from recombinant
CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
CC mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
CC dengue type 4 virus. The methods and compositions of the invention are
CC useful for fine tuning the attenuation and growth characteristics of
CC dengue virus vaccines for the prevention and/or treatment of dengue virus
CC infection. The present sequence is Dengue virus type 4 strain rDENV4 DNA
XX
SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 10; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 306 CCCATCTCTCAGAAATCCCTGCTGTGG 279

RESULT 7

AAD53910/C
ID AAD53910 standard; DNA; 10649 BP.

XX AC AAD53910;

XX 28-MAY-2003 (first entry)

XX Dengue virus type 4 strain 2A DNA.

XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.

XX Dengue virus.

XX Key Location/Qualifiers

FT CDS 102..10649
FT /*tag= a
FT /product= "DENV4 strain 2A protein"
FT mat_peptide 102..440
FT /*tag= c
FT /product= "Anchored capsid protein"
FT mat_peptide 102..398
FT /*tag= b
FT /product= "Viron capsid protein"
FT mat_peptide 441..938
FT /*tag= d
FT /product= "Membrane precursor protein"
FT mat_peptide 714..938
FT /*tag= e
FT /product= "Membrane protein"
FT mat_peptide 939..2423
FT /*tag= f
FT /product= "Envelope protein"
FT mat_peptide 2424..3479
FT /*tag= g
FT /product= "NS1 protein"
FT mat_peptide 3480..4133
FT /*tag= h
FT /product= "NS2A protein"
FT mat_peptide 4134..4523
FT /*tag= i
FT /product= "NS2B protein"
FT mat_peptide 4524..6377
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide 6378..6758
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide 6759..6827
FT /*tag= l
FT /product= "2K protein"
FT mat_peptide 6828..7562
FT /*tag= m

FT mat_peptide /product= "NS4B protein"
FT 7563..10262
FT /*tag= n
FT /product= "NS5 protein"

XX W0200295075-A1.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-US016308.

XX 22-MAY-2001; 2001US-0293049P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.

XX Whitehead SS, Murphy BR, Hanley KA;

XX WPI; 2003-120809/11.

XX P-PSDB; AAE35312.

XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.

XX Disclosure; Page 123-126; 246pp; English.

XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DENV4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain 2A DNA

XX Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 10; Length 10649;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 306 CCCATCTCTCAGAAATCCCTGCTGTGG 279

RESULT 8

AAD14605/C

ID AAD14605 standard; cDNA; 10717 BP.

XX AC AAD14605;

XX 11-SEP-2003 (revised)

XX 01-NOV-2001 (first entry)

XX Dengue virus (DENV)-2/3-VP1 chimeric cDNA.

XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.

XX Dengue virus; type II.

XX Dengue virus; type III.

XX Chimeric.

XX Key Location/Qualifiers

XX CDS 97..10266

XX /*tag= a

XX /product= "DEN-2/3-VP1 fusion protein"

XX W0200160847-A2.

XX

PD 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005142.
 XX
 PR 16-FEB-2000; 2000US-0182829P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
 XX WPI; 2001-497162/54.
 DR P-PSDB; AAE07984.
 XX
 XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 XX Example 2; Page 203-219; 470pp; English.
 XX
 XX The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present CDNA
 CC sequence encodes dengue virus (DEN)-2/3-VPI fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS3)-250 and the
 CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
 Query Match 89.3%; Score 25; DB 4; Length 10717;
 Best Local Similarity 89.3%; Pred. No. 0.52;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277
 RESULT 9
 AAT49303/c
 ID AAT49303 standard; cDNA; 10723 BP.
 XX
 AC AAT49303;
 XX
 XX 27-AUG-2003 (revised)
 DT 11-SEP-1997 (first entry)
 XX
 XX cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
 XX
 XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; ss.
 XX
 XX Dengue virus type 2 (strain 16681).
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 97. .10272
 FT /tag= a
 FT /product= "DEN-2 polyprotein
 FT /transl_except(pos:9208..9210, aa:Xaa)"
 FT /note= "Xaa = unknown amino acid"
 XX

PN WO9640933-A1.
 XX 19-DEC-1996.
 XX
 XX 06-JUN-1996; 96WO-US009209.
 XX
 XX 07-JUN-1995; 95US-00483292.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYMA-) UNIV MAHIDOL AT SALAYA.
 XX
 XX Bhamarapratvati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kinney R, Trent DW;
 XX WPI; 1997-052330/05.
 DR P-PSDB; AAW06590.
 XX
 XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadravalent vaccine for protecting against Dengue virus infection.
 XX
 XX Claim 23; Page 107-121; 261pp; English.
 XX
 XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
 CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, PDK
 CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence which
 CC -53, may be used in the production of a quadravalent vaccine which
 CC provides immunity against all four serotypes of dengue virus. The vaccine
 CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
 CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
 CC protect against infection by all four serotypes of dengue virus, DEN-1,
 CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue,
 CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
 CC to produce the recombinant protein products of the DNA constructs which
 CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;
 Query Match 89.3%; Score 25; DB 2; Length 10723;
 Best Local Similarity 89.3%; Pred. No. 0.52;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277
 RESULT 10
 AAT49304/c
 ID AAT49304 standard; cDNA; 10723 BP.
 XX
 AC AAT49304;
 XX
 XX 27-AUG-2003 (revised)
 DT 12-SEP-1997 (first entry)
 XX
 XX cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
 XX
 XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; ss.
 XX
 XX Dengue virus type 2 (strain 16681).
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 57
 FT mutation /tag= b
 FT /note= "C>T mutation"
 FT CDS 97. .10272
 FT /tag= a

Db 304 CCATCTCTTCAATATCCCTGCTGTGG 277
||||| ||| |||||||

RESULT 12
AAD14607/c
ID AAD14607 standard; cDNA; 10723 BP.
XX
AC AAD14607;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Wild-type, virulent DEN-2 16681 cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
OS Dengue virus; type II.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 16681 protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07986.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 252-268; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTTCAATATCCCTGCTGTGG 28
||||| ||| |||||||

Db 304 CCATCTCTTCAATATCCCTGCTGTGG 277
||||| ||| |||||||

RESULT 13
AAD14606/c
ID AAD14606 standard; cDNA; 10723 BP.
XX
AC AAD14606;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/4-VP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS Dengue virus; type IV.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/4-VP1 fusion protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07985.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 227-243; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/4-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 EDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCTCTTCAATATCCCTGCTGTGG 28
||||| ||| |||||||

Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 14
AAD14608/c
ID AAD14608 standard; cDNA; 10723 BP.

AC AAD14608;
XX
DT 01-NOV-2001 (first entry)
XX
DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; muten;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW ss.

OS Dengue virus; type II.
OS Synthetic.

XX
XX
XX Key Location/Qualifiers
FT mutation replace(57, C)
FT /*tag= b
FT CDS 97..10272
FT /*tag= a
FT /*product= "DEN-2 PDK-53 protein variant"
FT mutation replace(524, A)
FT /*tag= c
FT mutation replace(2055, C)
FT /*tag= d
FT mutation replace(2579, G)
FT /*tag= e
FT mutation replace(4018, C)
FT /*tag= f
FT mutation replace(5270, A)
FT /*tag= g
FT mutation replace(5547, T)
FT /*tag= h
FT mutation replace(6599, G)
FT /*tag= i
FT mutation replace(8571, C)
FT /*tag= j

XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX
XX P-PSDB; AAE07987.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 276-292; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic

CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, (E) membrane/membrane protein (prM) encoding region, an envelope
CC protein, (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region
XX
XX
SQ Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 4; Length 10723;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTCTTCAATATCCCTGCTGTGG 277

RESULT 15
ADN98025/c
ID ADN98025 standard; DNA; 10724 BP.

XX ADN98025;
XX
XX 29-JUL-2004 (first entry)
XX
XX Dengue Virus isolate New Guinea complete genome sequence.
DE
KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX Dengue virus.
XX
XX WO2004040263-A2.
XX
XX 13-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034823.
XX
XX 31-OCT-2002; 2002US-0422755P.
XX
XX 06-JUN-2003; 2003US-0476513P.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Wong SJ, Pei-Yong S;
XX
XX WPI; 2004-400223/37.

XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
XX reactive with antibody against WNV and cross-reactive with antibody
XX against a flavivirus, useful in diagnosing flavivirus infection caused by
XX DENV, WNV, JEV or SLEV.
XX
XX Disclosure; Fig 40; 212pp; English.

XX The invention relates to a diagnostic kit comprising at least one
XX isolated and purified polypeptide comprising a West Nile Virus (WNV)
XX envelope (E) protein or its immunogenic fragment having a native
XX conformation or non-denatured structure and that is reactive with
XX antibodies against WNV and cross-reactive with antibodies against a
XX flavivirus. The diagnostic kit is useful in diagnosing flavivirus
XX infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
XX the complete nucleotide sequence of the DENV isolate New Guinea.
XX
XX
SQ Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;
Query Match 89.3%; Score 25; DB 12; Length 10724;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 304 CCCATCTCTTCAATATATCCCTGCTGTGG 277

RESULT 16
AAD14609/c
ID AAD14609 standard; cDNA; 10756 BP.
XX
AC AAD14609;
XX
XX
DT 11-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/WN-PP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS West Nile virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10305
FT FT /tag= a
FT FT /product= "DEN-2/WN-PP1 fusion protein"
XX
PN WO200160847-A2.
XX
XX
PD 23-AUG-2001.
XX
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07988.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 6; Page 300-316; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/WN-PP1 fusion protein related to
CC the invention. This fusion protein contains DEN-2 16681 backbone and the
CC premembrane/membrane protein (ppm) and an envelope protein (E) from West
CC Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-
CC SEP-2003 to standardise OS field)
XX
SQ Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

Query Match 89.3%; Score 25; DB 4; Length 10756;
Best Local Similarity 89.3%; Pred. No. 0.52;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 304 CCCATCTCTTCAATATATCCCTGCTGTGG 277

RESULT 17
AAT75919/c
ID AAT75919 standard; DNA; 32 BP.
XX
XX AAT75919;
XX
DT 15-SEP-1997 (first entry)
XX
DE DEN-2 cloning/sequencing sense primer, D2-274.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
XX
XX Synthetic.
XX
XX WO9640933-A1.
XX
PD 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX WPI; 1997-052330/05.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Example; Page 100; 261pp; English.
XX
CC The sequences given in AAT75909-T76029 are primers which were used in the
CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the
CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises
CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.
CC The quadravalent vaccine of the invention comprises an attenuated Dengue
CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3
CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are
CC used to protect against infection by all four serotypes of dengue virus,
CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal
CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are
CC used to produce the recombinant protein products of the DNA constructs
CC which are used in the vaccines
XX
SQ Sequence 32 BP; 12 A; 7 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 83.6%; Score 23.4; DB 2; Length 32;
Best Local Similarity 85.7%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 31 CCCATCTCTTCAATATATCCCTGCTGTGG 4

RESULT 18
AAD14612/c
ID AAD14612 standard; cDNA; 10648 BP.

```
XX AAD14612;
AC
XX
XX 11-SEP-2003 (revised)
DT
XX 01-NOV-2001 (first entry)
DE
XX Wild-type, virulent DEN-4 1036 cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type IV.
OS
XX
XX Key Location/Qualifiers
FH 102..10265
FT /*tag= a
FT /product= "DEN-4 1036 protein"
XX WO200160847-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 16-FEB-2001; 2001WO-US005142.
PF
XX
XX 16-FEB-2000; 2000US-0182829P.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
PI WPI; 2001-497162/54.
XX P-PSDB; AAE07991.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 3; Page 373-389; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
SQ
Query Match 83.6%; Score 23.4; DB 4; Length 10648;
Best Local Similarity 85.7%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1 CCCATCTCTCCTCANNATCCCTCTGTGG 28
||||| ||| |||||
Db 306 CCCATCTTTTCAGAAATCCCTCTGTGG 279
|||||
RESULT 19
AAD14613/c
ID AAD14613 standard; cDNA; 10648 BP.
```

```
XX AAD14613;
AC
XX
XX 01-NOV-2001 (first entry)
DE
XX Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; mutein;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX ss.
XX
XX Dengue virus; type IV.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 102..10265
FT /*tag= a
FT /product= "DEN-4 PDK-48 protein variant"
XX WO200160847-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 16-FEB-2001; 2001WO-US005142.
PF
XX
XX 16-FEB-2000; 2000US-0182829P.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
PI WPI; 2001-497162/54.
XX P-PSDB; AAE07992.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 4; Page 397-413; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
SQ
Query Match 83.6%; Score 23.4; DB 4; Length 10648;
Best Local Similarity 85.7%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy 1 CCCATCTCTCCTCANNATCCCTCTGTGG 28
||||| ||| |||||
Db 306 CCCATCTTTTCAGAAATCCCTCTGTGG 279
|||||
RESULT 19
AAD14613/c
ID AAD14613 standard; cDNA; 10648 BP.
```

CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
 CC 48 times is designated as DEN-4 PDK-48 virus

XX Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
 SQ Query Match 83.6%; Score 23.4; DB 4; Length 10648;
 Best Local Similarity 85.7%; Pred. No. 2.7;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
 ||||| ||| ||||| ||||| |||||
 Db 306 CCCATCTCTTTCAGAAATCCCTGCTGTTGG 279

RESULT 20
 AAQ12787/c
 ID AAQ12787 standard; RNA; 10723 BP.

XX AC AAQ12787;
 XX DT 25-MAR-2003 (revised)
 DT 21-NOV-1991 (first entry)
 XX DE Dengue 2 virus genome.
 XX KW dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
 XX OS Dengue virus.

XX PH Location/Qualifiers
 FT CDS 97..10272
 FT /*tag= a
 FT 712..936
 FT /*tag= b
 FT /product= "M protein"
 FT 937..2421
 FT /*tag= c
 FT /product= "E protein"
 FT 2422..3477
 FT /*tag= d
 FT /product= "NS1"
 FT 3478..4131
 FT /*tag= e
 FT /product= "NS2A"
 FT 4132..4518
 FT /*tag= f
 FT /product= "NS2B"
 FT 4519..6375
 FT /*tag= g
 FT /product= "NS3"
 FT 6376..6825
 FT /*tag= h
 FT /product= "NS4a"
 FT 6826..7569
 FT /*tag= i
 FT /product= "NS4B"
 FT 7570..10269
 FT /*tag= j
 FT /product= "NS5"

XX FR2654113-A.
 XX 10-MAY-1991.
 XX 09-NOV-1989; 89FR-00914724.
 XX 09-NOV-1989; 89FR-00014724.
 XX (INSP) INST PASTEUR.
 XX Vincent D;
 XX Ivy JM, Nakano E, Clements D;

DR WPI: 1991-225002/31.
 DR P-PSDB; AAR13166.
 XX Detection and identification of Flaviviridae in biological sample - by
 FT amplifying consensus sequence then hybridisation opt. followed by typing,
 FT e.g. sequencing amplified prod.
 XX Disclosure; Fig 3; 24pp; French.
 XX The dengue 2 virus is an example of a member of the Flaviviridae which
 CC can be identified using the probe pair of the invention. A species-
 CC specific sequence can be amplified using the claimed oligonucleotides as
 CC primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
 CC which can be identified include Japanese encephalitis virus and yellow
 CC fever virus. (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
 SQ Query Match 83.6%; Score 23.4; DB 2; Length 10723;
 Best Local Similarity 85.7%; Pred. No. 2.7;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTGG 28
 ||||| ||| ||||| ||||| |||||
 Db 304 CCCATCTTTCAGTATCCCTGCTGTTGG 277

RESULT 21
 AAT47666/c
 ID AAT47666 standard; cDNA; 3381 BP.

XX AC AAT47666;
 XX DT 17-OCT-2003 (revised)
 DT 19-MAY-1997 (first entry)
 XX DE Dengue virus serotype 2 PR159/S1 mutant sequence.
 XX KW DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.
 XX OS Dengue virus; serotype 2.

XX PH Location/Qualifiers
 FT mutation 1216..1218
 FT /*tag= a
 FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
 FT is GAA (Glu) in wild-type PR159"
 FT mutation 1258..1260
 FT /*tag= b
 FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1
 FT is GTG (Val) in wild-type PR159"
 FT mutation 1762..1764
 FT /*tag= c
 FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
 FT is ATT (Ile) in wild-type PR159"
 FT mutation 1927..1929
 FT /*tag= d
 FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
 FT is AGT (Ser) in wild-type PR159"

XX WO9637221-A1.
 XX 28-NOV-1996.
 XX 24-MAY-1996; 96WO-US007627.
 XX 24-MAY-1995; 95US-00448734.
 PR 07-JUN-1995; 95US-00488807.
 PR 10-JUL-1995; 95US-00500469.
 XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
 XX Ivy JM, Nakano E, Clements D;

XX WPI; 1997-020938/02.
DR P-PSDB; AAW09409.
XX Sub-unit vaccine against flavivirus infection - contg. recombinant
PT envelope protein in secretable form, used for immunising against
PT flavivirus infection.
XX
PS Example 1; Fig 3A-D; 121pp; English.
XX
CC A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
CC conservative mutation in domain B of S1 that may be involved in the
CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of
CC the virus. The clone can be used to express recombinant secreted
CC polypeptides, comprising portions of the envelope protein (esp. domain B,
CC Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and
CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 77.9%; Score 21.8; DB 2; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTCTTTTAATATCCCTGCTGTGG 181
RESULT 22
AA25114/c
ID AA25114 standard; cDNA; 3381 BP.
XX
AC AA25114;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA.
XX
KW Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
XX
OS Dengue virus; serotype 2.
XX
FN WO9906068-A2.
XX
PD 11-FEB-1999.
XX
DF 27-JUL-1998; 98WO-US015447.
XX
PR 31-JUL-1997; 97US-00904227.
XX
PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX
FI Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
XX
DR WPI; 1999-153454/13.
DR P-PSDB; AAY05522.
XX
PT Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
PT 80% protein, useful for protecting against flavivirus, especially dengue
PT virus infections.
XX
PS Example 1; Fig 3A-D; 60pp; English.
XX
CC This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
CC (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
CC strain served as the source for DEN-2 genes used in the invention. A
CC vaccine for protecting against flavivirus infection comprises a dimeric
CC 80% E protein that has been secreted as a recombinant protein from a

CC eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
CC zipper domain through the homodimeric association of 2 leucine zipper
CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the
CC formation of a non-covalently associated four-helix bundle domain formed
CC upon association of two helix-turn-helix moieties attached to the C-
CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
CC efficiently secreted by recombinant cells, are easier to purify than
CC intracellular proteins, and generate a high titer neutralising antibody
CC response. The method is generally applicable to flaviviruses, in
CC particular dengue viruses such as DEN-2, where 80% E comprises amino
CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
Query Match 77.9%; Score 21.8; DB 2; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 208 CCCATCTCTTTTAATATCCCTGCTGTGG 181
RESULT 23
ADL98085/c
ID ADL98085 standard; DNA; 3381 BP.
XX
AC ADL98085;
XX
DT 18-NOV-2004 (first entry)
XX
DE Dengue virus, DEN-2, partial genome.
XX
KW Dengue virus; DEN-2; ss; Envelope protein; 80% E; membrane protein;
KW capsid protein; NS1 protein; Dengue haemorrhagic fever; DHF;
KW Dengue shock syndrome; DSS; flavivirus; vaccine.
XX
OS Dengue virus type 2; strain PR159/S1.
XX
FH Key Location/Qualifiers
FT CDS 1..3381
FT /tag= a
FT /product= "DEN-2 Capsid-membrane-envelope-NS1 proteins"
FT /partial
FT /note= "No stop codon shown"
XX
PN US2003175304-A1.
XX
PD 18-SEP-2003.
XX
PF 20-SEP-2002; 2002US-00247960.
XX
PR 31-JUL-1997; 97US-00904227.
PR 18-AUG-1999; 99US-00376463.
XX
PA (PETE/) PETERS I D.
PA (COLL/) COLLIER B G.
PA (MCDO/) MCDONELL M.
PA (IVYJ/) IVY J M.
PA (HARA/) HARADA K.
XX
PI Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;
XX
DR WPI; 2003-898503/82.
DR P-PSDB; ADL98086.
XX
XX Vaccine useful for protection against dengue virus infection, comprises a
XX dimeric 80% envelope, which has been secreted as a recombinantly produced
XX protein from Drosophila Schneider cells.
XX


```

PS Example 1; Fig 3; 31pp; English.
XX
CC The invention relates to a vaccine for protection against Flavivirus
CC infection comprising a dimeric 80% envelope (E), which has been secreted
CC as a recombinantly produced protein from Drosophila Schneider cells and
CC which represents the N-terminal 80% portion of the protein from residue 1
CC -395. Also included are a method for protecting a subject against a
CC Flavivirus, an immunogenic polypeptide comprising a dimeric 80% E, an
CC immunogenic composition for protection against Flavivirus infection
CC comprising the immunogenic polypeptide and a carrier, an immunodiagnostic
CC kit for detecting Flavivirus comprising the immunogenic polypeptide, a vector
CC host recombinant DNA expression system, a DNA sequence encoding the
CC immunogenic polypeptide and an immunodiagnostic kit for detecting
CC Flavivirus in a test subject. The dimeric 80% E products are envelope
CC proteins of serotypes comprising DEN-1, DEN-2, DEN-3 or DEN-4. The
CC Flavivirus is a dengue virus. The 80% E protein is produced as a dimer by
CC incorporating 2 different kinds of leucine zipper peptides or
CC incorporating a helix-turn-helix peptide, to encourage dimerisation. The
CC vaccine is useful for protection against dengue virus infection (e.g.
CC Dengue haemorrhagic fever, DHF, and Dengue shock syndrome, DSS). The
CC present sequence is the partial genomic sequence of the DEN-2 strain
CC PR159/S1 virus, encoding the capsid, membrane, envelope and NS1 proteins.
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 77.9%; Score 21.8; DB 11; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTTCANNATCCCTGCTGTGG 28
DB 208 CCCATCTTTTAAATATATATCCCTGCTGTGG 181

RESULT 24
ADQ28715/c
ID ADQ28715 standard; DNA; 3381 BP.
XX
AC ADQ28715;
XX
DT 26-AUG-2004 (first entry)
XX
DE Dengue virus viral capsid, prM, E and NS1 genes.
XX
KW virucide; vaccine; Flavivirus; dimeric 80%E; Drosophila Schneider cell;
KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
KW viral capsid; prM gene; E gene; NS1 gene; ds.
XX
OS Dengue virus.
XX
FH Key Location/Qualifiers
FT CDS 1..3381
FT FT /*tag= a
FT FT /product= "Dengue virus viral capsid, prM, E and NS1
FT FT polypeptide"
XX
PN US6749857-B1.
XX
XX 15-JUN-2004.
XX
PF 18-AUG-1999; 99US-00376463.
XX
PR 31-JUL-1997; 97US-00904227.
XX
XX (HAWAII) HAWAII BIOTECHNOLOGY GROUP INC.
XX
XX Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;
XX
XX WPI; 2004-438725/41.
XX
XX P-PSDB; ADQ28716.
XX
XX New vaccines for preventing or diagnosing infections caused by dengue
XX virus comprises a therapeutic amount of a dimeric 80%E protein secreted
PT

```

```

PT from Drosophila Schneider cells.
XX
PS Example 1; SEQ ID NO 2; 47pp; English.
XX
CC The invention describes a vaccine that generates a protective,
CC neutralising antibody response to a Flavivirus in a murine host. The
CC vaccine comprises a therapeutic amount of a dimeric 80%E, the dimeric
CC 80%E having been secreted as a recombinantly produced protein from
CC Drosophila Schneider cells, and where 80%E represents the N-terminal 80%
CC portion of the protein from residues 1-395. Also described are: an
CC immunogenic polypeptide comprising the dimeric 80%E cited above; an
CC immunogenic composition that generates a protective, neutralising
CC antibody response to a Flavivirus in a murine host, comprising the above
CC immunogenic polypeptide and a physiological carrier; a multivalent
CC immunodiagnostic kit for the detection of Flavivirus, comprising at least 2
CC of the above immunogenic polypeptides of at least 2 flaviviral serotypes;
CC and an immunodiagnostic kit for the detection of Flavivirus in a test
CC subject, comprising the above immunogenic or multivalent immunodiagnostic
CC polypeptide, a suitable support phase coated with dimeric 80%E, and
CC labeled antibodies immunoreactive to antibodies from the test subject.
CC The composition is useful for preventing or diagnosing infections caused
CC by dengue virus. This sequence encodes Dengue virus gene viral capsid,
CC prM, E and NS1 genes for Dengue virus strain PR159/S1 used as the source
CC of DEN-2 genes for the invention.
XX
SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 77.9%; Score 21.8; DB 12; Length 3381;
Best Local Similarity 82.1%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTTCANNATCCCTGCTGTGG 28
DB 208 CCCATCTTTTAAATATATATCCCTGCTGTGG 181

RESULT 25
ADG93313/c
ID ADG93313 standard; DNA; 15159 BP.
XX
AC ADG93313;
XX
DT 11-MAR-2004 (first entry)
XX
DE DEN2 (Tonga/74) cDNA plasmid P2.
XX
KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW dengue virus; delta30; attenuating mutation; humoral response;
KW cellular response; non-structural protein; structural protein;
KW dengue virus serotype; gene; ds; plasmid P2.
XX
OS Dengue virus type 2.
XX
XX WO2003092592-A2.
XX
PN 13-NOV-2003.
XX
PD 25-APR-2003; 2003WO-US013279.
XX
PF 03-MAY-2002; 2002US-0377860P.
XX
PR 23-DEC-2002; 2002US-0436500P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX Hanley K;
XX
XX WPI; 2004-022612/02.
XX
XX P-PSDB; ADG93314.
XX
XX
XX New tetravalent vaccine containing a common nucleotide deletion in the 3'
XX untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT

```

PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
PS Disclosure; SEQ ID NO 46; 181pp; English.
XX This invention relates to a novel immunogenic composition being
CC tetra-valent and containing a common nucleotide deletion in the 3',
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetra-valent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetra-valent vaccine, the new tetra-valent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC) structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN2 cDNA plasmid P2 which is related to the
CC invention.
XX
SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;
Query Match 77.9%; Score 21.8; DB 12; Length 15159;
Best Local Similarity 82.1%; Pred. No. 15;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 304 CCCATCTCTTTTAATATATCCCTGCTGTGG 277
RESULT 26
AA049305/c
ID AAT49305 standard; cDNA; 2394 BP.
XX
AC AAT49305;
XX
XX
DT 27-AUG-2003 (revised)
DT 15-SEP-1997 (first entry)
XX
XX
DE Nucleotide sequence of DEN-1 16007 PDK-13 vaccine virus.
XX
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
XX DHF; DSS; ss.
XX
OS Dengue virus type 2.
XX
XX WO9640933-A1.
XX
PD 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
XX Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
XX P-PSDB; AAW06592.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
XX quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 31; Page 172-176; 261pp; English.

XX This sequence represents the nucleotide sequence of one of the candidate
CC vaccine viruses of the invention. This sequence is based on the
CC nucleotide sequence encoding the polyprotein from dengue 2 virus, strain
CC 16681. The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B,
CC NS3, NS4A, NS4B and NS5 proteins. The quadravalent vaccine of the
CC invention comprises an attenuated Dengue virus clone, PDK-53, and a
CC chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-
CC 2/4 virus. The new quadravalent vaccines are used to protect against
CC infection by all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and
CC DEN-4, which can lead to dengue fever or fatal dengue haemorrhagic
CC fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the
CC recombinant protein products of the DNA constructs which are used in the
CC vaccines. (Updated on 27-AUG-2003 to correct QS field.)
XX
SQ Sequence 2394 BP; 752 A; 505 C; 622 G; 515 T; 0 U; 0 Other;
Query Match 72.1%; Score 20.2; DB 2; Length 2394;
Best Local Similarity 78.6%; Pred. No. 57;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
Db 115 CCCATCTAGCCAAATTCCTGCTGTGG 88
RESULT 27
AA051476/c
ID AA051476 standard; DNA; 10718 BP.
XX
XX AA051476;
XX
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-MAY-1994 (first entry)
XX
XX DEN1-S275/90 (ECACC V92042111) .
XX
XX Dengue haemorrhagic fever; DHF; dengue fever; DE; dengue shock syndrome;
XX DSS; DEN1 polypeptides; ss.
XX
XX Dengue virus type 2.
XX
XX
XX Key Location/Qualifiers
XX CDS 81..10271
XX /tag= a
XX misc_RNA 81..422
XX /tag= b
XX misc_RNA 123..422
XX /label= C
XX /tag= C
XX misc_RNA 423..695
XX /label= C'
XX /tag= d
XX misc_RNA 696..920
XX /label= Prem
XX /tag= e
XX misc_RNA 921..2402
XX /label= M
XX /tag= f
XX misc_RNA 2403..3464
XX /label= E
XX /tag= g
XX misc_RNA 3465..4112
XX /label= NS1
XX /tag= h
XX misc_RNA 4113..4499
XX /label= NS2A
XX /tag= i
XX misc_RNA 4500..6359
XX /label= NS2B
XX /tag= j
XX misc_RNA /label= NS3

```
FT misc_RNA      6360..6809
FT               /*tag= k
FT               /label= NS4A
FT misc_RNA      6810..7556
FT               /*tag= l
FT               /label= NS4B
FT misc_RNA      7557..10268
FT               /*tag= m
FT               /label= NS5
XX
XX WO9322440-A1.
XX
XX 11-NOV-1993.
XX
XX 28-APR-1993; 93WO-CA000182.
XX
XX 29-APR-1992; 92GB-00009243.
XX
XX (UYSI-) UNIV SINGAPORE NAT.
XX
XX Tan Y, Fu J, Tan B, Yap E, Chan Y;
XX
XX WPI; 1993-368799/46.
XX
XX P-PSDB; AAR43662.
XX
XX New Dengue virus type 1 strain - used to obtain prods. for detection,
XX diagnosis, vaccines and treatment involving virus.
XX
XX Claim 3; Page 20-34; 55pp; English.
XX
XX DEN1 virus, strain S275/90 was isolated from the serum of a dengue
XX haemorrhagic fever (DHF) patient. RNA was isolated from the virus and
XX used to prepare cDNA encoding DEN1 polypeptides. Dengue Virus Type 1
XX prods. can be used for detection, diagnosis, vaccines (inactivated form)
XX or treatment of DEN1 infections. The sequences given in AAO51477-86 are
XX oligonucleotides used to prepare cDNA fragments corresp. to Dengue virus
XX proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;
XX
XX Query Match 72.1%; Score 20.2; DB 2; Length 10718;
XX Best Local Similarity 78.6%; Pred. No. 72;
XX Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
XX ||||| || |||||
XX Db 288 CCCATCTAGCCAAATTCCTGCTGTGG 261
XX
XX RESULT 28
XX AAD14603/c
XX ID AAD14603 standard; cDNA; 10723 BP.
XX
XX AC AAD14603;
XX
XX 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VP chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
XX OS Dengue virus; type II.
XX OS Chimeric.
XX
XX Key Location/Qualifiers
XX FH 97..10272
XX FT /*tag= a
XX FT /product= "DEN-2/1-VP fusion protein"
XX

PN WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07982.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 155-170; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VP fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), pre-membrane/membrane protein (prM) and an envelope
XX protein (E) from wild-type DEN-1 15007 virus. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX
XX SQ Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;
XX
XX Query Match 72.1%; Score 20.2; DB 4; Length 10723;
XX Best Local Similarity 78.6%; Pred. No. 73;
XX Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
XX ||||| || |||||
XX Db 304 CCCATCTGCCAAATTCCTGCTGTGG 277
XX
XX RESULT 29
XX AAD14604/c
XX ID AAD14604 standard; cDNA; 10723 BP.
XX
XX AC AAD14604;
XX
XX 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VP chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
XX OS Dengue virus; type II.
XX OS Chimeric.
XX
XX Key Location/Qualifiers
XX FH 97..10272
XX FT /*tag= a
XX FT /product= "DEN-2/1-VP fusion protein"
XX
```

```
PN WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07983.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 179-195; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-W fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX SQ Sequence 10735 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 72.1%; Score 20.2; DB 4; Length 10723;
Best Local Similarity 78.6%; Pred. No. 73;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTCTCTTGG 28
Db 304 CCCATCTAGCCAAATTCCTCTCTTGG 277

RESULT 30
AAD14602/C
ID AAD14602 standard; cDNA; 10735 BP.
XX
XX AC AAD14602;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
XX
XX KW Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; muten;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX 88.
XX
XX OS Dengue virus; type 1.
XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX CDS 95..10273
XX /*tag= a
XX /*product= "DEN-1 PDK-13 protein variant"
XX /*replace(1123, T)
XX /*tag= b

mutation replace(1541, G)
mutation /*tag= c
mutation replace(1543, A)
mutation /*tag= d
mutation replace(1545, G)
mutation /*tag= e
mutation replace(1567, A)
mutation /*tag= f
mutation replace(1608, C)
mutation /*tag= g
mutation replace(2363, A)
mutation /*tag= h
mutation replace(2695, T)
mutation /*tag= i
mutation replace(2782, C)
mutation /*tag= j
mutation replace(3063, G)
mutation /*tag= k
mutation replace(6048, A)
mutation /*tag= l
mutation replace(6806, A)
mutation /*tag= m
mutation replace(7330, A)
mutation /*tag= n
mutation replace(9445, C)
mutation /*tag= o

WO200160847-A2.
23-AUG-2001.
16-FEB-2001; 2001WO-US005142.
16-FEB-2000; 2000US-0182829P.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
WPI; 2001-497162/54.
P-PSDB; AAE07981.
Chimeric flaviviruses that are avirulent and immunogenic, useful for
vaccinating against a range of dengue viruses.
Example 1; Page 130-146; 470pp; English.
The invention relates to avirulent, immunogenic flavivirus chimeras
comprising amino acid mutations in the non-structural proteins of a
flavivirus. Chimeric viruses containing the attenuation-mutated non-
structural genes of the virus are used as a backbone into which the
structural protein genes of a second flavivirus strain are inserted.
These chimeric viruses elicit pronounced immunogenicity but lack the
accompanying clinical symptoms of viral disease. Attenuated chimeric
flaviviruses are combined in a pharmaceutical composition to confer
simultaneous immunity against several strains of pathogenic flaviviruses
such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
flavivirus chimeras are also used as immunogens or multivalent vaccines
to confer simultaneous protection against infections. The present cDNA
sequence encodes dengue virus (DEN)-2/1-W fusion protein related to the
invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
comprising a valine at the non-structural protein (NS3)-250 and the
capsid protein (C), premembrane/membrane protein (prM) and an envelope
protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
(Updated on 11-SEP-2003 to standardise OS field)
Sequence 10735 BP; 3429 A; 2231 C; 2776 G; 2299 T; 0 U; 0 Other;
Query Match 72.1%; Score 20.2; DB 4; Length 10735;
Best Local Similarity 78.6%; Pred. No. 73;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

OY 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
|||||
Db 302 CCCATCTAGCCAAATTCCTGCTGTGG 275

RESULT 31

AD14601/c
ID AAD14601 standard; cDNA; 10735 BP.

AC AAD14601;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX

DE Wild-type, virulent DEN-1 16007 cDNA.

XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX

OS Dengue virus; type I.

XX Key Location/Qualifiers
FH 95..10273
FT CDS /*tag= a
FT /*product= "DEN-1 16007 protein"

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07980.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.

XX Example 1; Page 106-122; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-1 (DEN-1) 16007 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 10735 BP; 3432 A; 2232 C; 2774 G; 2297 T; 0 U; 0 Other;

Query Match 72.1%; Score 20.2; DB 4; Length 10735;

Best Local Similarity 78.6%; Pred. No. 73;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
|||||
Db 302 CCCATCTAGCCAAATTCCTGCTGTGG 275

RESULT 32

ADN98024/c

ID ADN98024 standard; DNA; 10735 BP.

XX

AC ADN98024;

XX 29-JUL-2004 (first entry)

XX Dengue Virus isolate WestPac complete genome sequence.

XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;

KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

XX Dengue virus.

XX WO2004040263-A2.

XX 13-MAY-2004.

XX 31-OCT-2003; 2003WO-US034823.

XX 31-OCT-2002; 2002US-0422755P.

XX 06-JUN-2003; 2003US-0476513P.

XX (HEAL-) HEALTH RES INC.

XX Wong SJ, Pei-Yong S;

XX WPI; 2004-400223/37.

XX GENBANK; U88535.

XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT reactive with antibody against WNV and cross-reactive with antibody
PT against a flavivirus, useful in diagnosing flavivirus infection caused by
PT DENV, WNV, JEV or SLEV.

XX Disclosure; Fig 39; 212pp; English.

XX The invention relates to a diagnostic kit comprising at least one
CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC envelope (E) protein or its immunogenic fragment having a native
CC conformation or non-denatured structure and that is reactive with
CC antibodies against WNV and cross-reactive with antibodies against a
CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
CC the complete nucleotide sequence of the DENV isolate WestPac.

XX Sequence 10735 BP; 3421 A; 2245 C; 2774 G; 2295 T; 0 U; 0 Other;

Query Match 72.1%; Score 20.2; DB 12; Length 10735;

Best Local Similarity 78.6%; Pred. No. 73;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CCCATCTCCTCANNATCCCTGCTGTGG 28
|||||

Db 302 CCCATCTAGCCAAATTCCTGCTGTGG 275

RESULT 33

ADG93317/c

ID ADG93317 standard; DNA; 2426 BP.

XX

AC ADG93317;

XX 11-MAR-2004 (first entry)

XX DEN1 (Puerto Rico/94) CME chimeric region DNA SeqID50.

XX immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
KW dengue virus; delta30; attenuating mutation; humoral response;
KW cellular response; non-structural protein; structural protein;
KW dengue virus serotype; gene; ds; plasmid P2.
XX
OS Dengue virus type 1.
XX
XX WO2003092592-A2.
PN
XX 13-NOV-2003.
XX
PD
XX 25-APR-2003; 2003WO-US013279.
XX
XX 03-MAY-2002; 2002US-0377860P.
PR
XX 23-DEC-2002; 2002US-0436500P.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
PI Hanley K;
PI
XX WPI; 2004-022612/02.
DR
XX P-PSDB; ADG93318.
DR
XX New tetravalent vaccine containing a common nucleotide deletion in the 3'
PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
PT of disease in humans caused by dengue virus, or for inducing immune
PT response.
XX
XX Disclosure; SEQ ID NO 50; 181pp; English.
XX
XX This invention relates to a novel immunogenic composition being
CC tetravalent and containing a common nucleotide deletion in the 3',
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC structural proteins present in each dengue virus serotype. The present
CC sequence is that of the DEN1 CME chimeric region DNA which is related to
CC the invention.
XX
SQ Sequence 2426 BP; 754 A; 509 C; 632 G; 531 T; 0 U; 0 Other;

Query Match 68.6%; Score 19.2; DB 12; Length 2426;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCATCTGTCANNATCCCTGCTGTGG 28
DB 308 CCACTAGCCAAATCTCTGCTGTGG 282
|||||
|||

RESULT 34
ADD47140
ID ADD47140 standard; DNA; 28564 BP.
XX
AC ADD47140;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Human gene U66061, SEQ ID NO 12830.
DE
XX Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW

KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
PR
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PA
XX Woolf C, D'urso D, Befort K, Costigan M;
PI
XX WPI; 2003-268312/26.
XX GENBANK; U66061.
DR
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX Example 1; Page; 1017pp; English.
PS
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
CC therapy). The sequence presented is a human DNA (described in Table 3 of
CC the specification) which encodes one of the polypeptides of the invention
CC which is differentially expressed during pain. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 28564 BP; 9286 A; 5444 C; 5773 G; 8061 T; 0 U; 0 Other;

Query Match 68.6%; Score 19.2; DB 10; Length 28564;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCATCTGTCANNATCCCTGCTGTGG 28
DB 17401 CCATGCTCAGACTCTCTGCTGTGG 17427
|||||
|||

RESULT 35
ADS73977
ID ADS73977 standard; DNA; 2237 BP.
XX
AC ADS73977;

```
XX 16-DEC-2004 (first entry)
XX Skeletal alpha-actin 3'-end nucleotide fragment.
XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
XX TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
XX vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
XX cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX Synthetic.
XX WO2004081040-A2.
XX 23-SEP-2004.
XX 11-MAR-2004; 2004WO-US007295.
XX 12-MAR-2003; 2003US-0454079P.
XX (ADVI-) ADVISYS INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Rabinovsky ED, Draghia-Akli R;
XX WPI; 2004-668935/65.
XX New isolated nucleic acid expression construct having a myogenic
XX promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
XX for treating diabetes, ischemic heart and cerebrovascular disease.
XX Claim 6; SEQ ID NO 5; 104pp; English.
XX The invention relates to an isolated nucleic acid expression construct
XX comprising a myogenic promoter, a nucleic acid sequence encoding an
XX insulin-like growth factor I (IGF-I) or its functional biological
XX equivalent, and a 3' untranslated region (3'UTR), which has in vivo
XX expression activity for the encoded IGF-I in a tissue. The myogenic
XX promoter in the isolated nucleic acid expression construct comprises a
XX transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
XX 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
XX The expression construct further comprises transfection-facilitating
XX vector system that is a plasmid, a viral vector, a liposome, or a
XX cationic lipid. The isolated nucleic acid expression construct also
XX comprises a transfection-facilitating polypeptide having a charged
XX polypeptide and/or poly-L-glutamate. The construct is useful in a method
XX for stimulating angiogenesis, or stimulating myogenesis, or elevating
XX levels of an angiogenic factor, or stimulating endogenous production of
XX an angiopoietin, or treating a muscular or vascular complications of
XX diabetes in a subject. The angiogenic factor comprises a vascular
XX endothelial growth factor (VEGF) or VEGF receptor. The methods and
XX compositions of the present invention are useful for the prevention
XX and/or treatment of diseases or conditions associated with aberrant
XX expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
XX heart disease, diabetic retinopathy and cerebrovascular disease. The
XX present sequence represents the nucleotide sequence of a skeletal alpha-
XX actin 3'-end fragment, a specific example of the 3'-UTR fragment used in
XX the nucleic acid expression construct of the invention.
XX SQ Sequence 2237 BP; 514 A; 567 C; 569 G; 587 T; 0 U; 0 Other;
Query Match 67.1%; Score 18.8; DB 13; Length 2237;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 ATCTGTCANNATCCCTGCTGTGG 28
Db 1925 ATCTCATCATCCTCCCTGCTGTGG 1949
RESULT 36
ADSV3973
ID ADS73973 standard; DNA; 5423 BP.
```

```
XX ADS73973;
XX 16-DEC-2004 (first entry)
XX Plasmid pAV2001 nucleotide sequence.
XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
XX TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
XX vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
XX cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX Synthetic.
XX WO2004081040-A2.
XX 23-SEP-2004.
XX 11-MAR-2004; 2004WO-US007295.
XX 12-MAR-2003; 2003US-0454079P.
XX (ADVI-) ADVISYS INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Rabinovsky ED, Draghia-Akli R;
XX WPI; 2004-668935/65.
XX New isolated nucleic acid expression construct having a myogenic
XX promoter, a nucleic acid sequence encoding IGF-Ile, and a 3'UTR, useful
XX for treating diabetes, ischemic heart and cerebrovascular disease.
XX Claim 11; SEQ ID NO 1; 104pp; English.
XX The invention relates to an isolated nucleic acid expression construct
XX comprising a myogenic promoter, a nucleic acid sequence encoding an
XX insulin-like growth factor I (IGF-I) or its functional biological
XX equivalent, and a 3' untranslated region (3'UTR), which has in vivo
XX expression activity for the encoded IGF-I in a tissue. The myogenic
XX promoter in the isolated nucleic acid expression construct comprises a
XX transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
XX 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
XX The expression construct further comprises transfection-facilitating
XX vector system that is a plasmid, a viral vector, a liposome, or a
XX cationic lipid. The isolated nucleic acid expression construct also
XX comprises a transfection-facilitating polypeptide having a charged
XX polypeptide and/or poly-L-glutamate. The construct is useful in a method
XX for stimulating angiogenesis, or stimulating myogenesis, or elevating
XX levels of an angiogenic factor, or stimulating endogenous production of
XX an angiopoietin, or treating a muscular or vascular complications of
XX diabetes in a subject. The angiogenic factor comprises a vascular
XX endothelial growth factor (VEGF) or VEGF receptor. The methods and
XX compositions of the present invention are useful for the prevention
XX and/or treatment of diseases or conditions associated with aberrant
XX expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
XX heart disease, diabetic retinopathy and cerebrovascular disease. The
XX present sequence represents the nucleotide sequence of a plasmid pAV2001,
XX a specific example of the isolated nucleic acid expression construct of
XX the invention.
XX SQ Sequence 5423 BP; 1219 A; 1475 C; 1474 G; 1255 T; 0 U; 0 Other;
Query Match 67.1%; Score 18.8; DB 13; Length 5423;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4 ATCTGTCANNATCCCTGCTGTGG 28
Db 2858 ATCTCATCATCCTCCCTGCTGTGG 2882
RESULT 37
```

```
AAQ32352
ID AAQ32352 standard; DNA; 5674 BP.
XX
AC AAQ32352;
XX
DT 25-MAR-2003 (revised)
DT 22-APR-1993 (first entry)
XX
DE MAGE-1 nucleic acid.
XX
KW melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3881..4711
FT /*tag= a
XX
XX WO9220356-A1.
XX
XX PD 26-NOV-1992.
XX
XX PF 22-MAY-1992; 92WO-US004354.
XX
XX PR 23-MAY-1991; 91US-00705702.
XX
XX PR 09-JUL-1991; 91US-00728838.
XX
XX PR 23-SEP-1991; 91US-00764364.
XX
XX PR 12-DEC-1991; 91US-00807043.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van pel A, De Plaen E;
XX PI Lurquin C, Chomez P, Traversari C;
XX
XX DR WPI; 1992-415460/50.
XX
XX PT Nucleic acid mol. encoding a human tumor rejection antigen precursor -
XX PT useful as an immunostimulant in a vaccine for treating and preventing
XX PT cancers, also useful in diagnosis.
XX
XX PS Disclosure; Page 71-73; 142pp; English.
XX
XX CC The sequences given in AAQ32352-69 represent a new family of genes
XX CC referred to as melanoma antigens (MAGE). The cDNAs of this gene family
XX CC were identified during the isolation of the antigen E gene. The MAGE
XX CC cDNAs, when tested, did not transfer expression of antigen E, but they
XX CC did show substantial homology to the antigen E cDNA sequence. The MAGE
XX CC cDNAs share a certain degree of homology with each other and are expressed
XX CC in tumor cells including several types of human tumor cells as well as
XX CC in human tumors. MAGE expression is not restricted to melanomas. MAGE
XX CC refers to a family of tumor rejection antigen precursors. The antigens
XX CC resulting from these genes are referred to as MAGE TRAs or melanoma
XX CC antigen tumor rejection antigens. See also AAQ32351. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX
XX SQ Sequence 5674 BP; 1277 A; 1644 C; 1568 G; 1185 T; 0 U; 0 Other;
XX
XX Query Match 67.1%; Score 18.8; DB 2; Length 5674;
XX Best Local Similarity 80.0%; Pred. No. 2.8e+02;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CCCATCTCNCANNATCCCTGCTGT 25
XX Db 1897 CTCATCTGTGAGAAATCCCTGCTGT 1921
XX
XX RESULT 38
XX AAQ72477
XX ID AAQ72477 standard; DNA; 5674 BP.
XX
XX AC AAQ72477;
XX
XX DT 25-MAR-2003 (revised)
XX DT 22-APR-1993 (first entry)
XX
XX DE MAGE-1 gene.
XX
XX KW Tumor rejection antigen; vaccine; cancer; MAGE-1 gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US5925729-A.
XX
XX PD 20-JUL-1999.
XX
XX PF 02-MAY-1994; 94US-00142368.
XX
XX
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DT 25-MAR-2003 (revised)
DT 22-JUN-1995 (first entry)
XX
DE Tumour rejection antigen MAGE-1 encoding DNA.
XX
KW Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3; cancer;
KW cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3881..4711
FT /*tag= a
XX
XX PN WO9423031-A1.
XX
XX PD 13-OCT-1994.
XX
XX PF 17-MAR-1994; 94WO-US002877.
XX
XX PR 26-MAR-1993; 93US-00037230.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;
XX PI WPI; 1994-333192/41.
XX
XX DR New tumour rejection antigen precursor MAGE3 - useful in treatment and
XX PT diagnosis of cancer.
XX
XX PS Example 26; Page 59; 105pp; English.
XX
XX CC AAQ72477 is the DNA sequence which encodes melanoma antigen-1 (MAGE-1).
XX CC Another melanoma antigen MAGE-3 is encoded by AAQ72470, this is a tumour
XX CC rejection antigen precursor. Melanomas characterised by the expression of
XX CC MAGE-3 can be detected, or monitored, by contacting a test sample with an
XX CC agent that can recognise MAGE-3. The melanoma can be treated by the
XX CC administration of cytolytic T cells specific for the complex of antigen D
XX CC (the mature rejection antigen derived from MAGE-3) and a human leucocyte
XX CC antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;
XX
XX Query Match 67.1%; Score 18.8; DB 2; Length 5674;
XX Best Local Similarity 80.0%; Pred. No. 2.8e+02;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CCCATCTCNCANNATCCCTGCTGT 25
XX Db 1897 CTCATCTGTGAGAAATCCCTGCTGT 1921
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XX RESULT 39
XX AAQ84113
XX ID AAX84113 standard; DNA; 5674 BP.
XX
XX AC AAX84113;
XX
XX DT 08-SEP-1999 (first entry)
XX
XX DE MAGE-1 gene.
XX
XX KW Tumour rejection antigen; vaccine; cancer; MAGE-1 gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US5925729-A.
XX
XX PD 20-JUL-1999.
XX
XX PF 02-MAY-1994; 94US-00142368.
XX
XX
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Search completed: July 31, 2005, 13:54:50
Job time : 236 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:00:46 ; Search time 1717.5 Seconds
(without alignments)
620.553 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccattctcannatccctgtgtgg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.4	72.9	1040	9	AG407066 Mus muscu
2	19.8	70.7	476	9	CL336324 RPC144_26
3	19.2	68.6	287	2	BB338318 BB338318
4	19.2	68.6	453	8	AO517624 HS 5140_B
5	19.2	68.6	481	5	EX109154 EX109154
6	19.2	68.6	511	7	CN675425 AO963B06-
7	19.2	68.6	577	9	CN690447 OXAB564TH
8	19.2	68.6	646	6	CD443887 EL01N0432
9	19.2	68.6	659	9	AG063981 Pan trogl
10	19.2	68.6	681	9	AG291906 Mus muscu
11	19.2	68.6	740	9	AG345215 Mus muscu
12	19.2	68.6	936	9	CL980943 OsiFCC035
13	19.2	68.6	938	9	CG232800 OGB2120TV
14	19.2	68.6	952	9	CG456461 PUJW63TD
15	19.2	68.6	961	9	CNS06EAT T3 end of
16	19.2	68.6	1018	9	CG456420 PUJW63TB
17	19.2	68.6	1139	8	CC187707 CH261-33N
18	19.2	68.6	2314	3	BC026893 Mus muscu
19	18.8	67.1	413	2	BF723268 mab30a01.
20	18.8	67.1	445	7	CF546284 lae70c10.
21	18.8	67.1	463	4	BI048424 MB4-TN011
22	18.8	67.1	923	9	CL116046 ISB1-63A2
23	18.8	67.1	990	9	AL149041 Anopheles
24	18.8	67.1	1137	9	CL025440 CH216-21K

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C	36	18.6	66.4	315	9	CR405165
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C	58	18.6	66.4	625	6	CA371379
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C	93	18.6	66.4	2562	9	CL962411
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C	95	18.6	66.4	4508	3	AK044502
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c 98	18.4	65.7	474	2	AW184935	se83h10.y	c 171	18.2	65.0	1416	9	CL648708	CH213-191
c 99	18.4	65.7	488	5	BP069231	BP069231	c 172	18.2	65.0	2526	3	AK047577	Mus muscu
c 100	18.4	65.7	508	8	AQ531444	RPCI-11-3	c 173	18	64.3	470	1	AJ828855	AJ828855
c 101	18.4	65.7	633	8	AQ020115	CJT-HSP-2	c 174	18	64.3	612	2	BF664792	602117715
c 102	18.4	65.7	718	7	CF888204	ama8tc-24	c 175	18	64.3	631	1	AL896204	AL896204
c 103	18.2	65.0	255	2	BB497890	BB497890	c 176	18	64.3	656	5	EX770566	EX770566
c 104	18.2	65.0	282	2	BB080784	BB080784	c 177	18	64.3	691	9	CNS03E4R	AL239940 Tetraodon
c 105	18.2	65.0	320	1	AI821851	nr38e03.x	c 178	18	64.3	713	5	BT779987	BT779987
c 106	18.2	65.0	320	1	AI826991	wk55c07.x	c 179	18	64.3	732	5	BQ028610	BQ028610
c 107	18.2	65.0	320	2	BF855145	RC3-FN020	c 180	18	64.3	866	7	CR421332	CR421332
c 108	18.2	65.0	321	1	AA635855	nr38e03.s	c 181	18	64.3	868	7	CR422895	CR422895
c 109	18.2	65.0	328	1	AI821103	nr38e03.y	c 182	18	64.3	890	5	EX691574	EX691574
c 110	18.2	65.0	401	9	CE402683	tigr-g88-	c 183	17.8	63.6	225	7	CF483205	CF483205
c 111	18.2	65.0	409	4	BG900352	HOA37-1-G	c 184	17.8	63.6	264	1	AV361891	AV361891
c 112	18.2	65.0	463	1	AI972423	w39e06.x	c 185	17.8	63.6	278	7	CF431363	CF431363
c 113	18.2	65.0	477	5	EX645883	DREZP781M	c 186	17.8	63.6	300	1	AV176398	AV176398
c 114	18.2	65.0	478	8	AQ559205	HS-2069B	c 187	17.8	63.6	300	6	C29822	C29822
c 115	18.2	65.0	490	7	CF139319	UI-HF-CB0	c 188	17.8	63.6	300	6	C33214	C33214
c 116	18.2	65.0	514	7	CF141511	UI-HF-CB0	c 189	17.8	63.6	373	6	BY630265	BY630265
c 117	18.2	65.0	529	8	AQ435078	HS-5114 B	c 190	17.8	63.6	386	6	BY582838	BY582838
c 118	18.2	65.0	543	7	CF860905	peZ0001G	c 191	17.8	63.6	404	6	CA910371	CA910371
c 119	18.2	65.0	548	9	CE632872	tigr-g88-	c 192	17.8	63.6	444	2	BB776803	BB776803
c 120	18.2	65.0	559	8	AQ560496	HS-2069B	c 193	17.8	63.6	456	2	BF411402	BF411402
c 121	18.2	65.0	562	7	CF122893	UI-HF-CB0	c 194	17.8	63.6	472	8	AQ526076	AQ526076
c 122	18.2	65.0	566	7	CF122893	UI-HF-CB0	c 195	17.8	63.6	499	4	BJ749870	BJ749870
c 123	18.2	65.0	572	7	CN984289	53244-126	c 196	17.8	63.6	518	7	CF440110	CF440110
c 124	18.2	65.0	580	7	CN975703	25590-125	c 197	17.8	63.6	520	2	AW564688	AW564688
c 125	18.2	65.0	582	6	CD832213	BN40-062H	c 198	17.8	63.6	532	4	BI502040	BI502040
c 126	18.2	65.0	585	6	CD836930	BN45-050H	c 199	17.8	63.6	533	4	BM141332	BM141332
c 127	18.2	65.0	594	9	CE598373	tigr-g88-	c 200	17.8	63.6	551	6	CB521458	CB521458
c 128	18.2	65.0	597	2	BF731559	maB8c08.	c 201	17.8	63.6	554	8	AQ546787	AQ546787
c 129	18.2	65.0	614	6	CA697619	wk4-pk00	c 202	17.8	63.6	571	9	CE448016	CE448016
c 130	18.2	65.0	630	5	BX085619	BX085619	c 203	17.8	63.6	579	6	CA187308	CA187308
c 131	18.2	65.0	638	6	CD835575	BN45-045P	c 204	17.8	63.6	613	4	BJ650386	BJ650386
c 132	18.2	65.0	641	5	EX085620	EX085620	c 205	17.8	63.6	616	6	CA108118	CA108118
c 133	18.2	65.0	647	9	AG041617	Pan trogl	c 206	17.8	63.6	616	8	BH822692	BH822692
c 134	18.2	65.0	652	7	BE584928	1-11G-ZO	c 207	17.8	63.6	617	6	CA743704	CA743704
c 135	18.2	65.0	654	5	BU238152	D801-13c0	c 208	17.8	63.6	625	7	CF113314	CF113314
c 136	18.2	65.0	661	6	BY733962	BY733962	c 209	17.8	63.6	626	8	BH835207	BH835207
c 137	18.2	65.0	672	6	CD355410	UI-M-PY0-	c 210	17.8	63.6	631	6	CA106744	CA106744
c 138	18.2	65.0	676	6	CD837009	BN45-050L	c 211	17.8	63.6	634	6	CA092088	CA092088
c 139	18.2	65.0	678	9	CE119987	tigr-g88-	c 212	17.8	63.6	638	7	CF449306	CF449306
c 140	18.2	65.0	687	7	CF146763	UI-HF-CB0	c 213	17.8	63.6	650	8	AZ414986	AZ414986
c 141	18.2	65.0	687	7	CF146837	UI-HF-CB0	c 214	17.8	63.6	666	6	CA914280	CA914280
c 142	18.2	65.0	701	6	CF722915	UI-M-GH0-	c 215	17.8	63.6	670	6	CA089948	CA089948
c 143	18.2	65.0	711	7	CF831705	UCRCR01.0	c 216	17.8	63.6	676	6	CB525542	CB525542
c 144	18.2	65.0	715	5	BU055491	UI-M-F00-	c 217	17.8	63.6	698	6	CA188826	CA188826
c 145	18.2	65.0	719	6	CD836858	BN45-050D	c 218	17.8	63.6	710	6	CD210780	CD210780
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c 147	18.2	65.0	731	6	CD837681	BN45-053D	c 220	17.8	63.6	738	7	CV045059	CV045059
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c 149	18.2	65.0	737	6	CD837090	BN45-051A	c 222	17.8	63.6	782	9	BX154563	BX154563
c 150	18.2	65.0	744	9	AG518630	Mus muscu	c 223	17.8	63.6	783	9	BX991431	BX991431
c 151	18.2	65.0	753	6	CB942622	AGENCOURT	c 224	17.8	63.6	794	9	CC919031	CC919031
c 152	18.2	65.0	754	7	CO560325	AGENCOURT	c 225	17.8	63.6	876	8	AZ672551	AZ672551
c 153	18.2	65.0	760	7	CN183954	UCRCS04.0	c 226	17.8	63.6	904	9	CNS03QVT	CNS03QVT
c 154	18.2	65.0	765	9	EX146761	Danio rer	c 227	17.8	63.6	916	2	BF125779	BF125779
c 155	18.2	65.0	772	6	CD835746	BN45-0461	c 228	17.8	63.6	922	9	CNS03HPV	CNS03HPV
c 156	18.2	65.0	784	6	CB521390	UI-M-GH0-	c 229	17.8	63.6	934	9	CNS04KRQ	CNS04KRQ
c 157	18.2	65.0	796	2	BF234751	602028578	c 230	17.8	63.6	960	2	BF310272	BF310272
c 158	18.2	65.0	801	7	CN537128	UI-M-HS0-	c 231	17.8	63.6	1000	9	CNS05BNN	CNS05BNN
c 159	18.2	65.0	806	2	BB640931	Cr12.1.M1	c 232	17.8	63.6	1044	5	BX380603	BX380603
c 160	18.2	65.0	814	7	CF746305	UI-M-GV0-	c 233	17.8	63.6	1127	7	CK212951	CK212951
c 161	18.2	65.0	818	7	CN187169	UCRCS05.0	c 234	17.8	63.6	1181	6	CD256455	CD256455
c 162	18.2	65.0	850	8	AQ888455	HS-3144A	c 235	17.6	62.9	127	7	CN283098	CN283098
c 163	18.2	65.0	868	1	AU118188	AU118188	c 236	17.6	62.9	185	9	CR181138	CR181138
c 164	18.2	65.0	913	3	CR713394	Tetraodon	c 237	17.6	62.9	227	2	BB150743	BB150743
c 165	18.2	65.0	926	3	CR688659	Tetraodon	c 238	17.6	62.9	228	1	AA755629	AA755629
c 166	18.2	65.0	936	3	CF681377	Tetraodon	c 239	17.6	62.9	272	8	AQ932827	AQ932827
c 167	18.2	65.0	1001	9	CNS05BPQ	Tetraodon	c 240	17.6	62.9	277	8	CE510117	CE510117
c 168	18.2	65.0	1101	9	CNS053A3	Tetraodon	c 241	17.6	62.9	280	8	AQ534695	AQ534695
c 169	18.2	65.0	1101	9	CNS0500V	Tetraodon	c 242	17.6	62.9	288	1	AA832894	AA832894
c 170	18.2	65.0	1201	3	CR674997	Tetraodon	c 243	17.6	62.9	288	1	AV311433	AV311433

244	17.6	62.9	295	8	BZ708794	BZ708794	OGEAK07TM	317	17.6	62.9	561	8	AZ900645	AZ900645	RPCI-24-1
245	17.6	62.9	297	2	BB092807	BB092807	BB092807	318	17.6	62.9	566	2	BE264616	BE264616	601192401
246	17.6	62.9	308	1	AL678860	AL678860	AL678860	C 319	17.6	62.9	567	7	CF356892	CF356892	maj50d02.
247	17.6	62.9	313	7	CR157636	CR157636	CR157636	C 320	17.6	62.9	567	7	CN297008	CN297008	170004706
248	17.6	62.9	330	7	CR774620	CR774620	DRF2p469D	321	17.6	62.9	571	4	BJ581270	BJ581270	BJS81270
249	17.6	62.9	336	6	CB488304	CB488304	omykttcho	322	17.6	62.9	571	8	AQ083692	AQ083692	HS 5478 B
250	17.6	62.9	354	4	BM368760	BM368760	EBem08 SQ	323	17.6	62.9	581	5	BP367826	BP367826	BP367826
251	17.6	62.9	367	4	BJ185424	BJ185424	BJ185424	C 324	17.6	62.9	582	4	BJ160499	BJ160499	BJ160499
252	17.6	62.9	377	5	BY072808	BY072808	BY072808	C 325	17.6	62.9	582	5	BP304995	BP304995	BP304995
253	17.6	62.9	385	2	BE102618	BE102618	UI-R-BT1-	C 326	17.6	62.9	582	5	BP345651	BP345651	BP345651
254	17.6	62.9	395	7	W20853	W20853	mb93g01.r1	C 327	17.6	62.9	584	4	BJ703733	BJ703733	BJ703733
255	17.6	62.9	395	2	BE695322	BE695322	CM0-BT079	C 328	17.6	62.9	585	8	AZ298569	AZ298569	RPCI-23-1
256	17.6	62.9	403	7	BJ185880	BJ185880	BJ185880	C 329	17.6	62.9	589	4	BJ168746	BJ168746	BJ168746
257	17.6	62.9	409	7	N26768	N26768	YX96e07.s1	C 330	17.6	62.9	591	7	CN496742	CN496742	Mdfw2022P
258	17.6	62.9	410	2	AW471015	AW471015	X280C12.x	C 331	17.6	62.9	594	4	BJ203989	BJ203989	BJ203989
259	17.6	62.9	424	2	AW443421	AW443421	EST308351	C 332	17.6	62.9	595	5	BX878488	BX878488	BX878488
260	17.6	62.9	425	5	BY449493	BY449493	BY449493	C 333	17.6	62.9	595	6	CB510113	CB510113	sealwh50
261	17.6	62.9	426	2	AW670518	AW670518	114588 MA	C 334	17.6	62.9	602	8	AQ787000	AQ787000	HS 3156 B
262	17.6	62.9	432	1	AI030199	AI030199	UI-R-C0-i	C 335	17.6	62.9	603	1	AI898646	AI898646	EST26809
263	17.6	62.9	432	2	BF742332	BF742332	QV0-BT086	C 336	17.6	62.9	603	8	AQ527450	AQ527450	RPCI-11-3
264	17.6	62.9	439	4	EG553669	EG553669	gac26d05.	C 337	17.6	62.9	607	7	CK617767	CK617767	m10106.Y
265	17.6	62.9	440	9	CR833204	CR833204	GR0AA66D	C 338	17.6	62.9	608	9	CR827504	CR827504	GR0AA59B
266	17.6	62.9	443	4	BI809329	BI809329	F004G02 O	C 339	17.6	62.9	609	4	BJ670376	BJ670376	BJ670376
267	17.6	62.9	447	2	BE020385	BE020385	sm43e12.y	C 340	17.6	62.9	609	4	BJ680048	BJ680048	BJ680048
268	17.6	62.9	448	1	AV746072	AV746072	AV746072	C 341	17.6	62.9	609	6	CB006128	CB006128	VVC030B07
269	17.6	62.9	449	4	BJ159898	BJ159898	BJ159898	C 342	17.6	62.9	610	6	CB005324	CB005324	VVC01F07
270	17.6	62.9	453	2	BB832344	BB832344	BB832344	C 343	17.6	62.9	610	6	CB174553	CB174553	OR A03 1
271	17.6	62.9	454	6	CB174223	CB174223	OR 2037H0	C 344	17.6	62.9	611	1	AI774264	AI774264	EST25459
272	17.6	62.9	457	7	CN580920	CN580920	MgfW2030N	C 345	17.6	62.9	611	5	BP766564	BP766564	BP766564
273	17.6	62.9	461	6	CD012422	CD012422	VVC015F05	C 346	17.6	62.9	612	4	BJ593311	BJ593311	BJ593311
274	17.6	62.9	470	2	BF602125	BF602125	267283 MA	C 347	17.6	62.9	613	4	BG063794	BG063794	H3012H04-
275	17.6	62.9	473	2	BE208075	BE208075	267283 MA	C 348	17.6	62.9	613	7	CV105571	CV105571	AGENCOURT
276	17.6	62.9	478	4	BJ162329	BJ162329	BJ162329	C 349	17.6	62.9	614	8	CC432260	CC432260	PUEGGL2TD
277	17.6	62.9	478	4	BJ645569	BJ645569	BJ645569	C 350	17.6	62.9	616	1	AI484751	AI484751	EST243012
278	17.6	62.9	480	1	AI899277	AI899277	EST268720	C 351	17.6	62.9	617	2	AW991452	AW991452	RC1-BN000
279	17.6	62.9	485	6	CB174266	CB174266	OR 2039E0	C 352	17.6	62.9	622	5	BW261307	BW261307	603503133
280	17.6	62.9	487	8	AQ810987	AQ810987	HS-5379 A	C 353	17.6	62.9	624	4	BJ045677	BJ045677	BJ045677
281	17.6	62.9	489	2	AS357525	AS357525	40541 MAR	C 354	17.6	62.9	625	4	BJ581422	BJ581422	BJ581422
282	17.6	62.9	490	7	CF787790	CF787790	856432 MA	C 355	17.6	62.9	627	4	BJ176200	BJ176200	BJ176200
283	17.6	62.9	491	6	CD013352	CD013352	VVC015F05	C 356	17.6	62.9	631	8	BH103391	BH103391	RPCI-24-3
284	17.6	62.9	493	2	AW251072	AW251072	2822269.3	C 357	17.6	62.9	635	4	BI811892	BI811892	B006810 O
285	17.6	62.9	494	8	CC052388	CC052388	SALK 0172	C 358	17.6	62.9	635	4	BM635532	BM635532	170006875
286	17.6	62.9	495	7	CR369447	CR369447	CR369447	C 359	17.6	62.9	635	6	CD002581	CD002581	EST0618 N
287	17.6	62.9	497	5	BP164740	BP164740	BP164740	C 360	17.6	62.9	636	5	BU364642	BU364642	603790533
288	17.6	62.9	500	8	B59918	B59918	CIT-HSP-347	C 361	17.6	62.9	643	9	AG131494	AG131494	Pan trogl
289	17.6	62.9	501	4	BJ161528	BJ161528	BJ161528	C 362	17.6	62.9	647	9	CG298566	CG298566	CGX8337TH
290	17.6	62.9	502	1	AA117598	AA117598	mp69a01.r	C 363	17.6	62.9	648	4	BI295863	BI295863	UI-R-DK0-
291	17.6	62.9	503	7	CK918645	CK918645	P3fmgc 00	C 364	17.6	62.9	651	6	CB174279	CB174279	OR 2039H0
292	17.6	62.9	506	5	BQ041243	BQ041243	g435809.Y	C 365	17.6	62.9	651	7	CN385782	CN385782	LB2TR0411
293	17.6	62.9	507	4	BI203533	BI203533	EST521573	C 366	17.6	62.9	654	4	BI204681	BI204681	EST522721
294	17.6	62.9	507	4	BI207288	BI207288	EST525328	C 367	17.6	62.9	655	5	BU425140	BU425140	603954486
295	17.6	62.9	507	4	BI211164	BI211164	EST529204	C 368	17.6	62.9	656	6	CB124937	CB124937	K-EST0173
296	17.6	62.9	515	4	BJ671149	BJ671149	BJ671149	C 369	17.6	62.9	657	2	BE251365	BE251365	601116219
297	17.6	62.9	517	4	BI294245	BI294245	UI-R-DK0-	C 370	17.6	62.9	660	1	AJ453558	AJ453558	AJ453558
298	17.6	62.9	518	8	BZ189347	BZ189347	CH230-329	C 371	17.6	62.9	664	6	CD462263	CD462263	SAL 40 HO
299	17.6	62.9	521	4	BJ193820	BJ193820	BJ193820	C 372	17.6	62.9	666	4	BM717237	BM717237	UI-E-DW1-
300	17.6	62.9	523	1	AI897247	AI897247	EST266606	C 373	17.6	62.9	666	5	BU041797	BU041797	PP Lra001
301	17.6	62.9	531	6	CB148275	CB148275	K-EST0204	C 374	17.6	62.9	667	1	AI748769	AI748769	8b61905.Y
302	17.6	62.9	534	6	CB174541	CB174541	OR H01 1	C 375	17.6	62.9	668	4	BI285605	BI285605	UI-R-CW0-
303	17.6	62.9	535	6	CB150261	CB150261	K-EST0206	C 376	17.6	62.9	670	2	BE251294	BE251294	601107804
304	17.6	62.9	540	4	BM438882	BM438882	S37497 MA	C 377	17.6	62.9	671	4	BJ078278	BJ078278	BJ078278
305	17.6	62.9	540	7	CK436213	CK436213	GQ0042.BR	C 378	17.6	62.9	672	7	CO237732	CO237732	W80073.B2
306	17.6	62.9	540	8	BZ868106	BZ868106	CH240 237	C 379	17.6	62.9	673	2	BE267182	BE267182	601190545
307	17.6	62.9	542	1	AA041112	AA041112	24378 CD4	C 380	17.6	62.9	673	5	AX666297	AX666297	AX666297
308	17.6	62.9	545	4	BJ695231	BJ695231	BJ695231	C 381	17.6	62.9	673	8	BQ345577	BQ345577	RPC111-11
309	17.6	62.9	550	5	BP266903	BP266903	BP266903	C 382	17.6	62.9	675	6	CA483164	CA483164	LUP12006E
310	17.6	62.9	551	8	AZ587888	AZ587888	1M0395D20	C 383	17.6	62.9	680	5	BU117314	BU117314	603138774
311	17.6	62.9	553	1	AU279438	AU279438	AU279438	C 384	17.6	62.9	682	2	BB180184	BB180184	BB180184
312	17.6	62.9	554	5	BP266570	BP266570	BP266570	C 385	17.6	62.9	682	7	CK759065	CK759065	atr02-lms
313	17.6	62.9	554	7	CK547931	CK547931	svk00 002	C 386	17.6	62.9	683	4	BJ170166	BJ170166	BJ170166
314	17.6	62.9	557	6	CD711716	CD711716	VVC01F07	C 387	17.6	62.9	683	5	BX866678	BX866678	BX866678
315	17.6	62.9	559	2	BP203599	BP203599	QV1865615	C 388	17.6	62.9	683	8	BZ153963	BZ153963	CH230-396
316	17.6	62.9	560	2	AW373824	AW373824	QV18-BT053	C 389	17.6	62.9	685	4	BG077234	BG077234	H3012H04-

C 390	17.6	62.9	689	2	BF2339512	BM140272	601906604	463	17.6	62.9	891	5	BM919599	BM919599	AGENCOURT
C 391	17.6	62.9	691	4	BM140272	OHC-65 Ge		464	17.6	62.9	891	9	CG297942	CG297942	CG3DY43TH
C 392	17.6	62.9	694	1	BM140272	BJ603137		465	17.6	62.9	896	9	CG305429	CG305429	OGWAB90TV
C 393	17.6	62.9	694	9	CG687873	CG687873	ZMMBB029	C 466	17.6	62.9	901	5	BQ943305	BQ943305	AGENCOURT
C 394	17.6	62.9	698	5	BF705132	BF705132		C 467	17.6	62.9	907	2	BF311349	BF311349	AGENCOURT
C 395	17.6	62.9	699	7	CG385777	CG385777	LE2T0410	C 468	17.6	62.9	912	4	BG394469	BG394469	601896749
C 396	17.6	62.9	700	1	AI1486585	AI1486585	EST244906	469	17.6	62.9	917	9	CG992745	CG992745	ZUAHS69TV
C 397	17.6	62.9	703	4	BJ592856	BJ592856		470	17.6	62.9	918	9	CG114753	CG114753	PUJFN33TD
C 398	17.6	62.9	704	8	CC170157	CC170157	I195C05.9	471	17.6	62.9	923	9	CG242324	CG242324	OGW1024TH
C 399	17.6	62.9	706	4	BM347074	BM347074	AI_3A10.H	472	17.6	62.9	924	9	CNS02V5S	CNS02V5S	Tetraodon
C 400	17.6	62.9	707	8	CC170445	CC170445	I196R09.9	473	17.6	62.9	927	7	CO121032	CO121032	GR_EB02A
C 401	17.6	62.9	709	6	BY755552	BY755552	BY755552	474	17.6	62.9	931	5	BQ925134	BQ925134	AGENCOURT
C 402	17.6	62.9	712	5	BU279150	BU279150	CG3862734	C 475	17.6	62.9	938	9	CG320358	CG320358	OGWAD78TV
C 403	17.6	62.9	714	2	AW604480	AW604480	RC3-C7025	476	17.6	62.9	940	4	BG328959	BG328959	602428607
C 404	17.6	62.9	716	4	BM783695	BM783695	K-EST061	C 477	17.6	62.9	940	7	CNS023543	CNS023543	AGENCOURT
C 405	17.6	62.9	718	7	CN297009	CN297009	170005325	C 478	17.6	62.9	940	9	AG381101	AG381101	Mus muscu
C 406	17.6	62.9	719	4	BG028676	BG028676	602292843	C 479	17.6	62.9	947	9	CNS01U04	CNS01U04	Tetraodon
C 407	17.6	62.9	723	5	BX889819	BX889819		C 480	17.6	62.9	951	5	BQ880709	BQ880709	AGENCOURT
C 408	17.6	62.9	725	2	BE741158	BE741158	601593972	C 481	17.6	62.9	951	9	CG297953	CG297953	CG3DY43TV
C 409	17.6	62.9	726	4	BG647192	BG647192	EST508811	C 482	17.6	62.9	974	9	CC675627	CC675627	OGUKP32TV
C 410	17.6	62.9	728	7	KA38166	KA38166	GQ0082_TB	483	17.6	62.9	984	5	BU847463	BU847463	AGENCOURT
C 411	17.6	62.9	736	1	AU123805	AU123805	AU123805	484	17.6	62.9	1014	5	BX400988	BX400988	AGENCOURT
C 412	17.6	62.9	736	4	BG329293	BG329293	602428369	485	17.6	62.9	1019	4	BM454685	BM454685	AGENCOURT
C 413	17.6	62.9	737	7	CF765771	CF765771	CES001184	C 486	17.6	62.9	1030	8	CC213267	CC213267	CH261-115
C 414	17.6	62.9	737	8	BH330542	BH330542	CH230-94F	487	17.6	62.9	1031	6	CA487731	CA487731	AGENCOURT
C 415	17.6	62.9	743	8	CC091505	CC091505	CSU-K33.r	C 488	17.6	62.9	1052	9	CG389780	CG389780	ZMMBB057
C 416	17.6	62.9	745	9	AG611216	AG611216	Mus muscu	C 489	17.6	62.9	1055	8	CC259342	CC259342	CH261-164
C 417	17.6	62.9	747	4	BG445247	BG445247	GA_Ea002	490	17.6	62.9	1095	4	BM458217	BM458217	AGENCOURT
C 418	17.6	62.9	749	1	AJ514223	AJ514223	AJ514223	491	17.6	62.9	1160	8	CC2398015	CC2398015	CH261-66C
C 419	17.6	62.9	756	4	BM009562	BM009562	603630130	492	17.6	62.9	1163	4	BG617997	BG617997	602644871
C 420	17.6	62.9	756	5	BM943681	BM943681	UI-M-EHOP	493	17.6	62.9	1188	8	CC230053	CC230053	CH261-162
C 421	17.6	62.9	759	6	CD783348	CD783348	EST654709	494	17.6	62.9	1280	9	CG749913	CG749913	P044-2-CO
C 422	17.6	62.9	760	7	CF348492	CF348492	AGENCOURT	C 495	17.6	62.9	1464	9	AG456367	AG456367	Mus muscu
C 423	17.6	62.9	762	5	BU282598	BU282598	603600412	C 496	17.6	62.9	1892	3	AK035824	AK035824	Mus muscu
C 424	17.6	62.9	776	5	CL425240	CL425240	ZMMBB0543	C 497	17.6	62.9	2019	3	BC039779	BC039779	Mus muscu
C 425	17.6	62.9	781	7	CO879294	CO879294	BovGen.07	C 498	17.6	62.9	2082	3	BC024795	BC024795	Mus muscu
C 426	17.6	62.9	782	4	B1970761	B1970761	GMB30011B	C 499	17.4	62.1	155	2	BF411513	BF411513	UI-R-BT1-
C 427	17.6	62.9	784	6	CD655830	CD655830	AGENCOURT	500	17.4	62.1	170	1	AU307722	AU307722	AU307722
C 428	17.6	62.9	784	7	CF997918	CF997918	AGENCOURT								
C 429	17.6	62.9	785	2	BE377560	BE377560	601229748								
C 430	17.6	62.9	788	5	BF737773	BF737773	BF737773								
C 431	17.6	62.9	794	9	CL768358	CL768358	OR_BBA014								
C 432	17.6	62.9	798	9	CC599602	CC599602	ZMMBB040								
C 433	17.6	62.9	807	5	BU750277	BU750277	CH3#032_B								
C 434	17.6	62.9	807	7	CK000763	CK000763	AGENCOURT								
C 435	17.6	62.9	808	2	BE796639	BE796639	601592035								
C 436	17.6	62.9	810	7	CF875234	CF875234	tr1c008xc								
C 437	17.6	62.9	811	6	CA386663	CA386663	668305_NC								
C 438	17.6	62.9	816	1	AU125141	AU125141	AU125141								
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C 440	17.6	62.9	824	9	CH819111	CH819111	GR0AA47B								
C 441	17.6	62.9	825	6	CA322414	CA322414	UI-M-FXO-								
C 442	17.6	62.9	829	1	AU140324	AU140324	AU140324								
C 443	17.6	62.9	829	5	BP171468	BP171468	BP171468								
C 444	17.6	62.9	829	5	BQ042702	BQ042702	UI-M-EMO-								
C 445	17.6	62.9	833	7	CN330519	CN330519	AGENCOURT								
C 446	17.6	62.9	835	7	CO248253	CO248253	AGENCOURT								
C 447	17.6	62.9	837	9	CK109576	CK109576	Reverse B								
C 448	17.6	62.9	837	9	CG360275	CG360275	OG1BE17TV								
C 449	17.6	62.9	838	8	B2179405	B2179405	CH230-444								
C 450	17.6	62.9	842	4	BG748215	BG748215	602631215								
C 451	17.6	62.9	843	7	CO247163	CO247163	AGENCOURT								
C 452	17.6	62.9	846	9	CG930556	CG930556	ZMMBB054								
C 453	17.6	62.9	848	6	CB245315	CB245315	UI-M-FY0-								
C 454	17.6	62.9	851	4	B1101548	B1101548	602887347								
C 455	17.6	62.9	855	9	CG052027	CG052027	PUIIZ59TD								
C 456	17.6	62.9	857	8	B2265404	B2265404	CH230-375								
C 457	17.6	62.9	865	2	BE379174	BE379174	601238157								
C 458	17.6	62.9	872	9	CG360262	CG360262	OG1BE17TH								
C 459	17.6	62.9	875	2	BF530467	BF530467	602071702								
C 460	17.6	62.9	883	6	CA791310	CA791310	AGENCOURT								
C 461	17.6	62.9	887	5	BQ669108	BQ669108	AGENCOURT								
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ALIGNMENTS

RESULT 1	AG407066	1040 bp	DNA	linear	GSS 03-JUN-2004
LOCUS	AG407066	Mus musculus molossinus	DNA	clone:MSMg01-265P04.T7	genomic survey
DEFINITION	AG407066	sequence.			
ACCESSION	AG407066	GI:48049752			
VERSION	AG407066				
KEYWORDS	GSS.				
SOURCE	Mus musculus molossinus				
ORGANISM	Mus musculus molossinus				
REFERENCE	1	Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki Y.			
AUTHORS	BAC and Sequences of Library MSMg01				
TITLE	Unpublished				
REFERENCE	2 (bases 1 to 1040)				
AUTHORS	Hattori M., Toyoda A., Noguchi H., Kojima T. and Sakaki Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)				
COMMENT	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center. The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199				

e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : T7

LIBRARY

Vector : pBACE3.6

R.Site 1 : ECORI

R.Site 2 : ECORI

Location/Qualifiers

1. .1040

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/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMG01-265P04.T7"

/sex="male"

/tissue_type="mixture of kidney and spleen"

/clone_lib="MSMG01 Mouse Male BAC Library"

ORIGIN

Query Match 70.7%; Score 19.8; DB 9; Length 476;
Best Local Similarity 80.8%; Pred. No. 6.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTT 26

DB 326 CCATCTCTCTCTTACCCCTGCTGTT 301

ORIGIN

Query Match 72.9%; Score 20.4; DB 9; Length 1040;
Best Local Similarity 84.0%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CATCTCTCANNATCCCTGCTGTTG 27

DB 648 CTCTCTCTCAACATCCCTGCTGTTG 672

RESULT 2

CL336324/c

LOCUS

DEFINITION RPCI44_263K5.f RPCI-44 Sus scrofa genomic clone RPCI44_263K5,
genomic survey sequence.

ACCESSION CL336324

VERSION CL336324.1 GI:51388292

KEYWORDS GSS.

SOURCE Sus scrofa (pig)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 476)

AUTHORS Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
Beever,J.E. and Schook,L.B.

TITLE Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
Through Comparative Genomics

JOURNAL

COMMENT

Other GSSs: RPCI44_263K5.r

Contact: Lawrence B. Schook

Department of Animal Sciences

University of Illinois at Urbana Champaign

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 265 5326

Fax: 217 244 5617

Email: schook@uiuc.edu

Clones are derived from the porcine BAC library RPCI-44

(<http://www.bacpac.chori.org/porcine242.htm>). For BAC library

availability, please contact Pieter de Jong (pdejong@chori.org).

Clones may be purchased from BACPAC Resources

(<http://BACPACorders.chori.org>). This work was undertaken as part

of the International Swine Genome Sequencing Consortium by

University of Illinois at Urbana Champaign, USA with funds provided

by grant No. AG2002-34480-11828 from USDA-CSREES and

AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing

Initiative)

Plate: 263 row: K column: 5

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .476

/organism="Sus scrofa"

/mol_type="genomic DNA"

/strain="four pigs (breed: 37.5% Yorks Landrace and 25%

Meishan)"

FEATURES

source

FEATURES

source

1. .287

Location/Qualifiers

1. .287

/db_xref="taxon:9823"

/clone="RPCI44_263K5"

/sex="male"

/cell_type="blood"

/clone_lib="RPCI-44"

/note="Vector: pTARBAC2; Site 1: ECORI; Site 2: EcoRI;
porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match 70.7%; Score 19.8; DB 9; Length 476;
Best Local Similarity 80.8%; Pred. No. 6.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTT 26

DB 326 CCATCTCTCTCTTACCCCTGCTGTT 301

RESULT 3

BB338318/c

LOCUS

DEFINITION

BB338318 RIKEN full-length enriched, 10 days neonate cerebellum Mus
musculus cDNA clone B930012N10 3' similar to U13152 Mesocricetus
auratus guanine nucleotide-binding protein beta 5 (Gnbs) mRNA, mRNA
sequence.

ACCESSION BB338318

VERSION BB338318.1 GI:9047081

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 287)

AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fuhunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Konno,H., et al.)

JOURNAL

COMMENT

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermostabilization of thermolabile enzymes by

trehalose and its application for the synthesis of full length

cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Osawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

Location/Qualifiers

1. .287

colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 58.6%; Score 19.2; DB 5; Length 481;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTG 27
|||||
DB 401 CCCACTTCCACAGATCCAGCTGTTG 427

RESULT 6

CN675425/C

LOCUS CN675425 511 bp mRNA linear EST 17-MAY-2004
DEFINITION A0963B06-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A0963B06 IMAGE:30772817 5', mRNA sequence.

ACCESSION CN675425.1 GI:47441876

VERSION EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 511)

Sharov,A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.

Transcriptome analysis of mouse stem cells and early embryos

PLoS Biol. 1 (3), 410-419 (2003)

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: A0963 row: B column: 06

Seq primer: M13 Reverse

High quality sequence stop: 511

POLYA-No.

FEATURES

source

Location/Qualifiers
1..511
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
/db_xref="niaEST:A0963B06-5"
/db_xref="taxon:10090"
/clone="NIA:A0963B06 IMAGE:30772817"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
cells were plated at density 3x104/cm2, on gelatin-coated
plates and cultured for 48 hrs at 37 OC, 5% CO2. Culture
medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,

0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
beta-mercaptoethanol, 1000 U/ml IIF, 100 U/ml penicillin,
and 100 ug/ml streptomycin. Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGGAGCGCCCTTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker LL-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.7 kb. The library was
constructed by Yulan Piao."

ORIGIN

Query Match 68.6%; Score 19.2; DB 7; Length 511;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTTG 27
|||||
DB 234 CCCAGCTCATCAGATCCCTGCATTG 208

RESULT 7

CC690447

LOCUS

DEFINITION

CC690447 ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0482K08,
genomic survey sequence.

ACCESSION

CC690447.1 GI:32095223

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

1 (bases 1 to 577)

Whiteley,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other_GSSs: OGAAB64TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..577

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBMA0482K08"

/clone_lib="ZM 0.7 1.5 KB"

/note="vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 577;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy 2 CCATCTCNCANNATCCCTGCTGTGG 28
Db 146 CCTGCTGTCAGCATCCCTGCAGTGG 172

RESULT 8
CD443887 646 bp mRNA linear EST 03-JUN-2003
LOCUS EL01N04132D03.b Endosperm_4 Zea mays cDNA, mRNA sequence.
ACCESSION CD443887
VERSION CD443887.1 GI:31359530
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 646)
Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,
Larkins, B., Beckett, P. and Messing, J.
Characterization of the maize endosperm transcriptome and its
comparison to the rice genome
Genome Res. 14 (10), 1932-1937 (2004)
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Wakeman Institute, Rutgers University
190 Freelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@wakeman.rutgers.edu
Seq primer: T3.
FEATURES
source
1..646
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 4"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 68.6%; Score 19.2; DB 6; Length 646;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 276 CCGATGTCATCATTCATCCCGCTGTG 302

RESULT 9
AG063981/c
LOCUS AG063981 659 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-052019.F, genomic survey sequence.
ACCESSION AG063981
VERSION AG063981.1 GI:16615783
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 626 CCCACCTCCACAGCATCCCGCTGTG 600

RESULT 10
AG291906/c
LOCUS AG291906 681 bp DNA linear GSS 02-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone: MSMg01-067B08.TJ, genomic survey
sequence.
ACCESSION AG291906
VERSION AG291906.1 GI:47864860
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 681)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Teukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Teukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source
1..659
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-052019.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 68.6%; Score 19.2; DB 9; Length 659;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 626 CCCACCTCCACAGCATCCCGCTGTG 600

FEATURES
source
1..681
Location/Qualifiers
/organism="Mus musculus molossinus"

```

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.

FEATURES
source
1..659
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-052019.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 68.6%; Score 19.2; DB 9; Length 659;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 626 CCCACCTCCACAGCATCCCGCTGTG 600

FEATURES
source
1..681
Location/Qualifiers
/organism="Mus musculus molossinus"

ORIGIN
Query Match 68.6%; Score 19.2; DB 9; Length 659;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTG 27
Db 276 CCGATGTCATCATTCATCCCGCTGTG 302

FEATURES
source
1..659
Location/Qualifiers
/organism="Mus musculus molossinus"

Qy 2 CCATCTCNTCANNATCCCTGCTGTGG 28

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES

Location/Qualifiers
1..938
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB0752D15"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 938;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCATCTCCTCANNATCCCTGCTGTGG 28
Db 51 CCTGCTGTCAGCATCCCTGCAGTTGG 77

RESULT 14

CG456461/c
LOCUS 952 bp DNA linear GSS 17-SEP-2003
DEFINITION FUIJW63TDB ZM 0.6 1.0 KB Zea mays genomic clone ZMMB7a0600K05,
genomic survey sequence.

ACCESSION CG456461
VERSION CG456461.1 GI:34841461

KEYWORDS GSS.
SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 952)

AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

TITLE Maize Genomics Consortium

JOURNAL Unpublished (2003)

COMMENT Other_GSSs: FUIJW63TDB

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

FEATURES

Location/Qualifiers
1..952
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB7a0600K05"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: pCF4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 952;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCATCTCCTCANNATCCCTGCTGTGG 28
Db 895 CCTGCTGTCAGCATCCCTGCAGTTGG 869

RESULT 15

CNS06EAJ/c
LOCUS 961 bp DNA linear GSS 17-JUN-2001

DEFINITION T3 end of clone AR0AA020A08 of library AR0AA from strain CBS 732 of

Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL394865

VERSION AL394865.1 GI:12146083

KEYWORDS GSS.

SOURCE Zygosaccharomyces rouxii

ORGANISM Zygosaccharomyces rouxii

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

REFERENCE 1 (bases 1 to 961)

AUTHORS Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G.,

Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,

de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Lorente, B.,

Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Potier, S.,

Saurin, W., Tekai, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,

Wincker, P. and Weissbach, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

PUBMED 11152876

REFERENCE 2 (bases 1 to 961)

AUTHORS de Montigny, J., Straub, M., Potier, S., Tekai, F., Dujon, B.,

Wincker, P., Artiguenave, F. and Souciet, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 8.

JOURNAL Zygosaccharomyces rouxii

MEDLINE FEBS Lett. 487 (1), 52-55 (2000)

PUBMED 20584718

REFERENCE 3 (bases 1 to 961)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,

2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia

lactis var. lactis, Kluyveromyces hanseni var. hanseni, Pichia sorbitophila,

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.

FEATURES

Location/Qualifiers

1..961

/organism="Zygosaccharomyces rouxii"

/mol_type="genomic DNA"

/strain="CBS 732"

/db_xref="taxon:4956"

/clone="AR0AA020A08"

/clone_lib="AR0AA"

/notes="end : T3"

misc_feature <3..>419

/note="similar to Saccharomyces cerevisiae ORF YNL289w [

PCU1; cyclin, GI/S-specific]"

/evidence=not_experimental

ORIGIN

Query Match 68.6%; Score 19.2; DB 9; Length 961;

Best Local Similarity 77.8%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCATCTCCTCANNATCCCTGCTGTGG 27

Db 431 CCTAGCTCATAGTATCCCTGCTGTGG 405

```

RESULT 16
CG456420      1018 bp   DNA      linear      GSS 17-SEP-2003
LOCUS        PUIJW63TBB ZM 0.6-1.0_KB Zea mays genomic clone ZM6T0600K05,
DEFINITION   genomic survey sequence.
ACCESSION    CG456420
VERSION      CG456420.1 GI:34841420
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 1018)
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
              Bennetzen,J.
TITLE        Maize Genomics Consortium
JOURNAL      Unpublished (2003)
COMMENT      Other GSSs: PUIJW63TDB
              Contact: Cathy Whitelaw
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: TR
              Class: sheared ends.
FEATURES     Location/Qualifiers
              1..1018
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /strain="B73"
              /db_xref="taxon:4577"
              /clone="ZM6T0600K05"
              /clone_lib="ZM 0.6-1.0_KB"
              /notes="vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
              Cot selected genomic DNA library"
ORIGIN
Query Match      68.6%; Score 19.2; DB 9; Length 1018;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2  CCATCTCTCANNATCCCTGCTGTGG 28
      |||||
Db   603 CCTGCTGTCAGCATCCTGCGAGTTGG 629

RESULT 17
CG187707      1139 bp   DNA      linear      GSS 08-MAY-2003
LOCUS        CH261-33N7 Sp6.1 CH261 Gallus gallus genomic clone CH261-33N7,
DEFINITION   genomic survey sequence.
ACCESSION    CG187707
VERSION      CG187707.1 GI:30431607
KEYWORDS     GSS.
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 1139)
AUTHORS      Warren,W., Graves,T., Nardis,S. and Wilson,R.
              Gallus gallus BAC End Reads
              Unpublished (2003)
TITLE        Genome Sequencing Center
JOURNAL      Washington University School of Medicine
COMMENT      Contact: Richard K. Wilson
              Email: submissions@watson.wustl.edu
              Insert Length: 182000 Std Error: 0.00

```

```

Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 145
High quality sequence stop: 618.
Location/Qualifiers
1..1139
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-33N7"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/notes="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"

```

FEATURES

source

ORIGIN

```

Query Match      68.6%; Score 19.2; DB 8; Length 1139;
Best Local Similarity 77.8%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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```

Qy  2  CCATCTCTCANNATCCCTGCTGTGG 28
      |||||
Db   131 CCAGCTCATCTATATCTTGCTGTGG 157

```

RESULT 18

```

LOCUS        BC026893/c      2314 bp   mRNA      linear      HTC 19-NOV-2003
DEFINITION   Mus musculus downstream of Stk11, mRNA (cDNA clone IMAGE:3982045),
              with apparent retained intron.
ACCESSION    BC026893
VERSION      BC026893.1 GI:22268016
KEYWORDS     HTC.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE    1 (bases 1 to 2314)
AUTHORS      Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
              Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
              Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
              Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heideh,F.,
              Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
              Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
              Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
              Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
              Abramson,R.D., Mullahy,S.J., Bosak,S.A., McSwan,P.J.,
              McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
              Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
              Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
              Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
              Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
              Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
              Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
              Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
              Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
              Generation and initial analysis of more than 15,000 full-length
              human and mouse cDNA sequences
              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

```

REFERENCE

AUTHORS

2 (bases 1 to 2314)

Strausberg,R.

Direct Submission

Submitted (04-APR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

REMARK

COMMENT

ORIGIN

TITLE
JOURNAL

REFERENCE
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

AUTHORS
2 (bases 1 to 990)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

TITLE
JOURNAL

COMMENT
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
source
1. .990
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="18E03"
/clone_lib="NotreDame1"
/note="end : SP6"

ORIGIN

Query Match 67.1%; Score 18.8; DB 9; Length 990;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
|||||
Db 525 CCCATCTCGTCTTTGTCCTGCTGT 501
|||||

RESULT 24
CLO25440/c
LOCUS
DEFINITION
CH216-21K12.RM1.1 CH216 Xenopus tropicalis genomic clone
CH216-21K12, genomic survey sequence.

ACCESSION
CLO25440
VERSION
CLO25440.1 GI:40468154
KEYWORDS
GSS.

ORGANISM
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
1 (bases 1 to 1137)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.

TITLE
JOURNAL

COMMENT
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGAGGA
Class: BAC ends
High quality sequence start: 100
High quality sequence stop: 743.
Location/Qualifiers
1. .1137
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-21K12"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

FEATURES
source
1. .1137
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-21K12"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 67.1%; Score 18.8; DB 9; Length 1137;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CATCTCNCANNATCCCTGCTGTG 27
|||||
Db 596 CACCTCTCTTTATCCCTGCTGTG 572
|||||

RESULT 25
CG755418/c
LOCUS
DEFINITION
P051-1-C06.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.

ACCESSION
CG755418
VERSION
CG755418.1 GI:37981893
KEYWORDS
GSS.

ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE
1 (bases 1 to 2185)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)

JOURNAL
MEDLINE
PUBMED
22835951
12884007

COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
1. .2185
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN

Query Match 67.1%; Score 18.8; DB 9; Length 2185;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
|||||
Db 1447 CCCATCAGCTCAGGATCCCTGCTAT 1423
|||||

RESULT 26
BF655438
LOCUS
DEFINITION
279922 MARCH 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
BF655438
VERSION
BF655438.1 GI:11920555
KEYWORDS
EST.

ORGANISM
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
1 (bases 1 to 231)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,

Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCGTCACGACG

Plate: 76 row: J column: 8

Seq primer: ATTTAGTGACACTATAG.

Location/Qualifiers

1..231

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 3BOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

66.4%; Score 18.6; DB 2; Length 231;
Similarity 75.0%; Pred.No.2.1e+03;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 CCATCTCCTCANNATCCCTGCTGTGG 28 linear EST 13-NOV-1999
||| |||||
27 CCTGTCTTCACTTCGCTGCTGTGG 54

AV361516 239 bp mRNA linear EST 13-NOV-1999
AV361516 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 753042BD08 3' similar to D29639 Mouse embryonal carcinoma cell mRNA for 3-hydroxyacyl CoA dehydrogenase, mRNA sequence.
AV361516
AV361516.1 GI:6408804
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 239)

Konno,H., Akizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,T., Tateno,M., Tominaga,N., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamuro,T., Yasuniishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Konno,H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suhei-ro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsic.riken.jp, URL:http://genome.gsc.riken.jp/
Saeaki,N., Izawa,M., Watabiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci.U.S.A. 95 (7). 3455-3460 (1998)

Qy	1	CCCATCTCTCANNATCCCTGCTGTGG	28
Db	105	CTGTGCTCTTCACCTTCGCTGCTGTGG	78
RESULT 32			
LOCUS	AW354424	280 bp	linear
DEFINITION	36211 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.		EST 25-APR-2001
ACCESSION	AW354424		
KEYWORDS	AW354424.1 GI:6853414		
SOURCE	EST.		
ORGANISM	Bos taurus (cow)		
REFERENCE			
AUTHORS	Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keeler, J.W.		
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle		
JOURNAL	Genome Res. 11 (4), 626-630 (2001)		
MEDLINE	21180013		
PUBMED	11282978		
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. PCR Primers FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTCCCAGTCACGACG Plate: 23 row: O column: 11 Seq primer: ATTAGTGACACTATAG. Location/Qualifiers 1. .280 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone_lib="MARC 1BOV" /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."		
FEATURES			
source			
ORIGIN			
Query Match	66.4%;	Score 18.6;	DB 2; Length 280;
Best Local Similarity	75.0%;	Pred. No. 2.1e+03;	
Matches	21; Conservative	0; Mismatches	7; Indels 0; Gaps 0;
Qy	1	CCCATCTCTCANNATCCCTGCTGTGG	28
Db	112	CCTGTCTCTTCACCTTCGCTGCTGTGG	139
RESULT 33			
LOCUS	AV116369	285 bp	linear
DEFINITION	AV116369 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA		EST 30-JUN-1999
ACCESSION	AV116369		
VERSION	AV116369.1 GI:5298520		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		


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/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="multiple myeloma"
/clone_lib="myeloma (MYE) cDNA library"
/notes="Vector: Lambda Zap Express; Site 1: EcoRI; Site 2:
XhoI; Myeloma cells from multiple myeloma patients' bone
marrow were purified by magnetic cell sorting. mRNA were
purified and an oligo d(T)18 primer containing XhoI
restriction site was used to prime first strand synthesis
using M-MLV reverse transcriptase. To protect the cDNAs
from XhoI digestion in subsequent cloning step, the
nucleotide analogue 5-methyl-dCTP was added to the
nucleotide mixture and [a-32P]dATP was added to monitor
the quantity and quality of first strand synthesis. After
second-strand synthesis and blunting of cDNA termini,
EcoRI adapters were ligated, followed by kinase treatment
and digestion with XhoI. The cDNAs were then
size-fractionated using Sephacryl S-500 column and then
ligated into EcoRI and XhoI digested Lambda Zap Express
vector. The ligation product was packaged using Gigapack
II packaging extract. The library had primary titre of
approx. 1x106. Clones from the primary library were
randomly selected for single pass sequencing."

ORIGIN
Query Match 66.4%; Score 18.6; DB 2; Length 300;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 166 CCCATCTCTGCAACAGCCGCTGTGGTGG 139

RESULT 36
CR405165
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-876C05-026468,
genomic survey sequence.
CR405165
CR405165.1 GI:46945893
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL MEDLINE
22755829
PUBMED 12874060
REFERENCE
2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL MEDLINE
23117147
PUBMED 14756321
REFERENCE
3 Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
JOURNAL PUBMED
14682050
REFERENCE
4 (bases 1 to 315)
Strizhov,N., Rosso,M.G., Li,Y. and Weisshaar,B.
Direct Submission

JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T22E19. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .315
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/scotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 66.4%; Score 18.6; DB 9; Length 315;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 5 CCAATTTTACATTATCCCTGCTTTGG 32

RESULT 37
CO727823/c
LOCUS UMC-bend 0A02-024-d02 Day 16 Uterus from a pregnant animal bend Bos
taurus cDNA 3', mRNA sequence.
CO727823
CO727823.1 GI:50710853
EST.
Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 348)
Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
Roberts,R.M., Smith,M.F. and Youngquist,R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
Reproduction
Unpublished (2002)
Contact: DNA Core Facility (Bovine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573) 882-0428
Fax: (573) 884-5552
Email: bovine@rnet.missouri.edu
POLYA=Yes.
Location/Qualifiers
1. .348
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone_lib="bend"
/notes="Funding: The production of ESTs submitted in this
project was funded by USDA Grant MRI-2002-03476 entitled
'Bovine ESTs: Focus on Female Reproduction' to RS Prather,"

JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T22E19. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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1. .315
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/mol_type="genomic DNA"
/strain="Columbia 0"
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/scotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 66.4%; Score 18.6; DB 2; Length 300;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGG 28
|||||
Db 166 CCCATCTCTGCAACAGCCGCTGTGGTGG 139

RESULT 36
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genomic survey sequence.
CR405165
CR405165.1 GI:46945893
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL MEDLINE
22755829
PUBMED 12874060
REFERENCE
2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL MEDLINE
23117147
PUBMED 14756321
REFERENCE
3 Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)
JOURNAL PUBMED
14682050
REFERENCE
4 (bases 1 to 315)
Strizhov,N., Rosso,M.G., Li,Y. and Weisshaar,B.
Direct Submission

```

E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.rnet.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at 37 degrees with 10mcg of NotI-tag-dt18 oligonucleotide (GCTGCTCGCGCGC-tag-T18) and reverse transcribed at 37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uiowa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and Rnase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SpOkr6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dt18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SpOkr6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails,

genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's Bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core Facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Sifers NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG TISSUE=Day 16 Uterus from a pregnant animal TAG_SEQ=CAACGTGTG"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 348;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCATCTCTCANNATCCCTGCTGTGG 28
DB 208 CCGTCTCTTCACTTCGCTGCTGTGG 181

RESULT 38

BF601010 389 bp mRNA linear EST 25-APR-2001
LOCUS BF601010
DEFINITION B25865 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF601010
VERSION BF601010.1 GI:11698231
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 389)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Kaegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.

REFERENCE

Authors

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smitht@mail.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

Plate: 39 row: C column: 20

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:23:11 ; Search time 71.5 Seconds
(without alignments)
640.780 Million cell updates/sec

Title: US-10-085-944-1

Perfect score: 28

Sequence: 1 cccatctcannatccctgctgttgg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	21.8	77.9	3381	3	US-08-937-195-2
C 4	21.8	77.9	3381	3	US-08-915-152-1
C 5	21.8	77.9	3381	3	US-08-915-152-2
C 6	21.8	77.9	3381	4	US-09-376-463-2
C 7	21.8	77.9	3381	5	PCT-US96-07627-1
C 8	21.8	77.9	3381	5	PCT-US96-07627-2
C 9	20.2	72.1	10718	3	US-08-325-426B-1
C 10	18.8	67.1	5674	1	US-07-807-043B-8
C 11	18.8	67.1	5674	1	US-08-190-411A-1
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C 15	18.8	67.1	5674	3	US-08-967-727-8
C 16	18.8	67.1	5674	3	US-08-037-230D-8
C 17	18.8	67.1	5674	4	US-09-583-850-8
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C 19	18.8	67.1	5674	4	US-09-404-026-8
C 20	18.8	67.1	5674	4	US-09-312-464-8
C 21	18.8	67.1	5699	4	US-09-949-016-12445
C 22	18.8	67.1	5699	4	US-09-949-016-14430
C 23	18.8	67.1	5707	2	US-08-472-809B-8
C 24	18.8	67.1	5345	2	US-08-472-809B-7
C 25	18.6	66.4	601	4	US-09-949-016-198635
C 26	18.6	66.4	767677	4	US-09-949-016-12147
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C 56	17.6	62.9	103792	4	US-09-949-016-13553	Sequence 13553, A
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C 66	17.2	61.4	5498	4	US-09-561-818A-5	Sequence 5, Appli
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C 68	17.2	61.4	6204	4	US-09-561-818A-1	Sequence 1, Appli
C 69	17.2	61.4	20870	4	US-09-949-016-16017	Sequence 16017, A
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C 80	17	60.7	4629	3	US-08-717-294-41	Sequence 41, Appl
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106	17	60.7	9164	4	US-09-205-817A-2	Sequence 2, Appli	c 179	57.9	601	4	US-09-949-016-133991	Sequence 133991, A
107	17	60.7	9354	1	US-08-683-839B-4	Sequence 2, Appli	c 180	57.9	601	4	US-09-949-016-135034	Sequence 135034, A
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109	17	60.7	11933	3	US-09-470-618-13	Sequence 13, Appli	c 182	57.9	601	4	US-09-949-016-198749	Sequence 198749, A
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113	17	60.7	24070	4	US-09-949-016-16153	Sequence 16153, A	c 186	57.9	601	4	US-09-949-016-201613	Sequence 201613, A
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116	17	60.7	44998	4	US-09-949-016-12824	Sequence 12824, A	c 189	57.9	2171	4	US-09-876-527-1	Sequence 1, Appli
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126	17	60.7	154600	4	US-09-949-016-14757	Sequence 14757, A	c 199	57.9	3390	4	US-09-767-878-1	Sequence 1, Appli
127	16.8	60.0	222	4	US-09-513-999C-27632	Sequence 27632, A	c 200	57.9	4609	4	US-09-919-039-340	Sequence 340, App
128	16.8	60.0	981	4	US-09-543-681A-2168	Sequence 2168, Ap	c 201	57.9	4855	4	US-09-876-594-847	Sequence 847, App
129	16.8	60.0	9480	4	US-09-657-013-35	Sequence 35, Appli	c 202	57.9	4876	4	US-09-949-016-12790	Sequence 12790, A
130	16.8	60.0	10087	4	US-09-657-013-29	Sequence 29, Appli	c 203	57.9	4877	4	US-09-949-016-14084	Sequence 14084, A
131	16.8	60.0	85122	4	US-09-949-016-14693	Sequence 14693, A	c 204	57.9	10701	4	US-09-949-016-14375	Sequence 14375, A
132	16.8	60.0	94077	4	US-09-949-016-13635	Sequence 13635, A	c 205	57.9	111235	4	US-09-949-016-15328	Sequence 15328, A
133	16.8	60.0	119214	4	US-09-949-016-12507	Sequence 12507, A	c 206	57.9	139150	4	US-09-949-016-17398	Sequence 17398, A
134	16.8	60.0	154600	4	US-09-949-016-14757	Sequence 14757, A	c 207	57.9	139577	4	US-09-949-016-12879	Sequence 12879, A
135	16.6	59.3	222	1	US-08-248-474-88	Sequence 88, Appli	c 208	57.9	163662	4	US-09-949-016-12545	Sequence 12545, A
136	16.6	59.3	222	3	US-08-756-849-88	Sequence 88, Appli	c 209	57.9	163664	4	US-09-949-016-13546	Sequence 13546, A
137	16.6	59.3	324	4	US-08-155-106-29	Sequence 29, Appli	c 210	57.9	165651	4	US-09-949-016-13032	Sequence 13032, A
138	16.6	59.3	394	4	US-09-513-999C-3611	Sequence 3611, Ap	c 211	57.9	194714	4	US-09-949-016-11869	Sequence 11869, A
139	16.6	59.3	456	4	US-09-621-976-400	Sequence 400, App	c 212	57.9	196714	4	US-09-949-016-15474	Sequence 15474, A
140	16.6	59.3	491	4	US-09-270-767-12530	Sequence 12530, A	c 213	57.9	221958	4	US-09-949-016-12173	Sequence 12173, A
141	16.6	59.3	601	4	US-09-949-016-60003	Sequence 60003, A	c 214	57.9	221966	4	US-09-949-016-15498	Sequence 15498, A
142	16.6	59.3	601	4	US-09-949-016-69043	Sequence 69043, A	c 215	57.9	256171	4	US-09-949-016-12822	Sequence 12822, A
143	16.6	59.3	1106	1	US-08-389-668A-3	Sequence 3, Appli	c 216	57.9	256176	4	US-09-949-016-15524	Sequence 15524, A
144	16.6	59.3	1106	1	US-08-732-506-3	Sequence 3, Appli	c 217	57.9	276	2	US-08-273-146-46	Sequence 46, Appli
145	16.6	59.3	1106	5	PCT-US95-05768-3	Sequence 3, Appli	c 218	57.9	321	2	US-08-672-176A-2	Sequence 2, Appli
146	16.6	59.3	1395	3	US-08-806-263-1	Sequence 1, Appli	c 219	57.9	341	4	US-09-513-999C-17702	Sequence 17702, A
147	16.6	59.3	1764	4	US-09-799-451-602	Sequence 602, App	c 220	57.9	343	4	US-09-621-976-17847	Sequence 17847, A
148	16.6	59.3	2938	3	US-08-969-815-3	Sequence 3, Appli	c 221	57.9	447	3	US-08-579-940-1	Sequence 1, Appli
149	16.6	59.3	2938	3	US-09-120-025-3	Sequence 3, Appli	c 222	57.9	447	3	US-08-838-692-3	Sequence 3, Appli
150	16.6	59.3	2938	3	US-09-710-481-3	Sequence 3, Appli	c 223	57.9	489	4	US-09-621-976-2891	Sequence 2891, Ap
151	16.6	59.3	2938	4	US-09-553-875-3	Sequence 3, Appli	c 224	57.9	554	3	US-08-348-548-3	Sequence 3, Appli
152	16.6	59.3	2938	4	US-09-768-670-3	Sequence 3, Appli	c 225	57.9	554	5	PCT-US95-15716-3	Sequence 3, Appli
153	16.6	59.3	2938	4	US-09-796-286-3	Sequence 3, Appli	c 226	57.9	601	4	US-09-949-016-45560	Sequence 45560, A
154	16.6	59.3	3211	2	US-08-574-959A-8	Sequence 8, Appli	c 227	57.9	601	4	US-09-949-016-85912	Sequence 85912, A
155	16.6	59.3	3211	3	US-09-357-014-8	Sequence 8, Appli	c 228	57.9	601	4	US-09-949-016-85913	Sequence 85913, A
156	16.6	59.3	3225	4	US-09-799-451-238	Sequence 238, App	c 229	57.9	601	4	US-09-949-016-85914	Sequence 85914, A
157	16.6	59.3	3901	2	US-08-574-959A-6	Sequence 6, Appli	c 230	57.9	601	4	US-09-949-016-86476	Sequence 86476, A
158	16.6	59.3	3901	3	US-09-357-014-6	Sequence 6, Appli	c 231	57.9	601	4	US-09-949-016-192789	Sequence 192789, A
159	16.6	59.3	7409	4	US-09-949-016-12689	Sequence 12689, A	c 232	57.9	601	4	US-09-949-016-192790	Sequence 192790, A
160	16.6	59.3	7409	4	US-09-949-016-15978	Sequence 15978, A	c 233	57.9	601	4	US-09-949-016-198411	Sequence 198411, A
161	16.6	59.3	14485	4	US-09-876-216-3	Sequence 3, Appli	c 234	57.9	601	4	US-09-949-016-198412	Sequence 198412, A
162	16.6	59.3	24984	4	US-09-949-016-14950	Sequence 14950, A	c 235	57.9	601	4	US-09-949-016-198413	Sequence 198413, A
163	16.6	59.3	31166	4	US-09-949-016-13464	Sequence 13464, A	c 236	57.9	652	2	US-08-737-129A-7	Sequence 7, Appli
164	16.6	59.3	34363	4	US-09-949-016-16341	Sequence 16341, A	c 237	57.9	689	4	US-09-270-767-4849	Sequence 4849, Ap
165	16.6	59.3	86116	4	US-09-949-016-14766	Sequence 14766, A	c 238	57.9	689	4	US-09-270-767-20131	Sequence 20131, A
166	16.6	59.3	96866	4	US-09-949-016-13768	Sequence 13768, A	c 239	57.9	920	2	US-08-860-174A-3	Sequence 3, Appli
167	16.6	59.3	158735	4	US-09-949-016-11989	Sequence 11989, A	c 240	57.9	920	3	US-09-171-025-24	Sequence 24, Appli
168	16.6	59.3	158735	4	US-09-949-016-17130	Sequence 17130, A	c 241	57.9	920	4	US-09-742-693-28	Sequence 28, Appli
169	16.6	59.3	312474	4	US-09-949-016-17434	Sequence 17434, A	c 242	57.9	1017	4	US-09-902-540-7918	Sequence 7918, Ap
170	16.6	59.3	343352	4	US-09-949-016-13498	Sequence 13498, A	c 243	57.9	1120	3	US-08-851-190-4	Sequence 4, Appli
171	16.4	58.6	32358	4	US-09-949-016-15677	Sequence 15677, A	c 244	57.9	1494	4	US-09-302-540-8019	Sequence 8019, Ap
172	16.4	58.6	265038	4	US-09-949-016-15779	Sequence 15779, A	c 245	57.9	1692	3	US-09-421-017B-664	Sequence 664, App
173	16.2	57.9	440	4	US-09-621-976-11347	Sequence 11347, A	c 246	57.9	1706	2	US-08-860-174A-11	Sequence 11, Appli

C 247	16	57.1	1706	3	US-09-171-025-27	Sequence 27, Appl	C 320	15.8	56.4	44971	4	US-09-949-016-17049	Sequence 17049, A
C 248	16	57.1	1745	3	US-09-171-025-1	Sequence 1, Appl	C 321	15.8	56.4	46319	4	US-09-949-016-17526	Sequence 17526, A
C 249	16	57.1	1952	4	US-09-466-921-24	Sequence 24, Appl	C 322	15.8	56.4	46323	4	US-09-949-016-17526	Sequence 17526, A
C 250	16	57.1	2091	4	US-09-488-039A-5233	Sequence 5233, Ap	C 323	15.8	56.4	78125	4	US-09-949-016-16006	Sequence 16006, A
C 251	16	57.1	2154	3	US-09-488-856A-3	Sequence 3, Appl	C 324	15.8	56.4	99748	4	US-09-949-016-11990	Sequence 11990, A
C 252	16	57.1	2318	4	US-09-488-856A-3	Sequence 4687, Ap	C 325	15.8	56.4	99749	4	US-09-949-016-16518	Sequence 16518, A
C 253	16	57.1	2341	4	US-09-620-3120-423	Sequence 423, App	C 326	15.8	56.4	113538	4	US-09-949-016-16329	Sequence 16329, A
C 254	16	57.1	2343	2	US-09-031-392-1	Sequence 1, Appl	C 327	15.8	56.4	209210	4	US-09-949-016-15094	Sequence 15094, A
C 255	16	57.1	2343	3	US-09-299-549-1	Sequence 1, Appl	C 328	15.8	56.4	227390	4	US-09-949-016-12201	Sequence 12201, A
C 256	16	57.1	2343	3	US-09-610-417-1	Sequence 1, Appl	C 329	15.8	56.4	227391	4	US-09-949-016-13365	Sequence 13365, A
C 257	16	57.1	2968	4	US-09-949-016-131	Sequence 131, App	C 330	15.8	56.4	228896	4	US-09-949-016-17127	Sequence 17127, A
C 258	16	57.1	3455	4	US-10-009-332-31	Sequence 31, Appl	C 331	15.8	56.4	254405	4	US-09-949-016-14381	Sequence 14381, A
C 259	16	57.1	3462	4	US-10-009-332-30	Sequence 30, Appl	C 332	15.6	55.7	328	4	US-09-513-999C-3055	Sequence 3055, Ap
C 260	16	57.1	3464	4	US-10-009-332-26	Sequence 26, Appl	C 333	15.6	55.7	601	4	US-09-949-016-29682	Sequence 29682, A
C 261	16	57.1	3467	4	US-10-009-332-25	Sequence 25, Appl	C 334	15.6	55.7	601	4	US-09-949-016-29683	Sequence 29683, A
C 262	16	57.1	3467	4	US-10-009-332-29	Sequence 29, Appl	C 335	15.6	55.7	601	4	US-09-949-016-29825	Sequence 29825, A
C 263	16	57.1	3469	4	US-10-009-332-27	Sequence 27, Appl	C 336	15.6	55.7	601	4	US-09-949-016-29826	Sequence 29826, A
C 264	16	57.1	3470	4	US-10-009-332-28	Sequence 28, Appl	C 337	15.6	55.7	601	4	US-09-949-016-33606	Sequence 33606, A
C 265	16	57.1	3473	4	US-10-009-332-24	Sequence 24, Appl	C 338	15.6	55.7	601	4	US-09-949-016-63265	Sequence 63265, A
C 266	16	57.1	4149	4	US-09-799-451-820	Sequence 820, App	C 339	15.6	55.7	601	4	US-09-949-016-64735	Sequence 64735, A
C 267	16	57.1	5357	4	US-09-979-765-1	Sequence 1, Appl	C 340	15.6	55.7	601	4	US-09-949-016-65547	Sequence 65547, A
C 268	16	57.1	7825	4	US-09-949-016-14399	Sequence 14399, A	C 341	15.6	55.7	601	4	US-09-949-016-87236	Sequence 87236, A
C 269	16	57.1	8241	4	US-09-902-540-798	Sequence 798, App	C 342	15.6	55.7	601	4	US-09-949-016-105170	Sequence 105170, A
C 270	16	57.1	8285	3	US-09-732-025-3	Sequence 3, Appl	C 343	15.6	55.7	601	4	US-09-949-016-131729	Sequence 131729, A
C 271	16	57.1	9033	4	US-09-902-540-815	Sequence 815, App	C 344	15.6	55.7	601	4	US-09-949-016-137730	Sequence 137730, A
C 272	16	57.1	9723	1	US-08-083-590A-21	Sequence 21, Appl	C 345	15.6	55.7	601	4	US-09-949-016-147598	Sequence 147598, A
C 273	16	57.1	9723	3	US-08-532-384-21	Sequence 21, Appl	C 346	15.6	55.7	601	4	US-09-949-016-147599	Sequence 147599, A
C 274	16	57.1	11827	3	US-09-739-455-3	Sequence 3, Appl	C 347	15.6	55.7	601	4	US-09-949-016-157435	Sequence 157435, A
C 275	16	57.1	14967	4	US-09-949-016-15448	Sequence 15448, A	C 348	15.6	55.7	601	4	US-09-949-016-157436	Sequence 157436, A
C 276	16	57.1	15164	4	US-09-919-497-20	Sequence 20, Appl	C 349	15.6	55.7	601	4	US-09-949-016-157542	Sequence 157542, A
C 277	16	57.1	21721	4	US-09-269-939A-41	Sequence 41, Appl	C 350	15.6	55.7	601	4	US-09-949-016-157543	Sequence 157543, A
C 278	16	57.1	22976	4	US-09-269-939A-19	Sequence 19, Appl	C 351	15.6	55.7	601	4	US-09-949-016-160157	Sequence 160157, A
C 279	16	57.1	23187	4	US-09-499-522-1	Sequence 1, Appl	C 352	15.6	55.7	601	4	US-09-949-016-160158	Sequence 160158, A
C 280	16	57.1	26159	4	US-09-949-016-13040	Sequence 13040, A	C 353	15.6	55.7	601	4	US-09-949-016-161271	Sequence 161271, A
C 281	16	57.1	32278	4	US-09-949-016-12959	Sequence 12959, A	C 354	15.6	55.7	601	4	US-09-949-016-161272	Sequence 161272, A
C 282	16	57.1	49526	4	US-09-949-016-12959	Sequence 12959, A	C 355	15.6	55.7	601	4	US-09-949-016-188401	Sequence 188401, A
C 283	16	57.1	91279	4	US-09-949-016-15446	Sequence 15446, A	C 356	15.6	55.7	601	4	US-09-949-016-188402	Sequence 188402, A
C 284	16	57.1	92227	4	US-09-949-016-11929	Sequence 11929, A	C 357	15.6	55.7	601	4	US-09-949-016-198904	Sequence 198904, A
C 285	16	57.1	92232	4	US-09-949-016-15421	Sequence 15421, A	C 358	15.6	55.7	601	4	US-09-949-016-198905	Sequence 198905, A
C 286	16	57.1	95122	4	US-09-949-016-17235	Sequence 17235, A	C 359	15.6	55.7	816	4	US-09-949-016-200143	Sequence 200143, A
C 287	16	57.1	112132	3	US-09-741-150-3	Sequence 3, Appl	C 360	15.6	55.7	816	4	US-09-248-796A-7077	Sequence 7077, Ap
C 288	16	57.1	112132	4	US-10-160-187-3	Sequence 3, Appl	C 361	15.6	55.7	938	4	US-09-843-472-2	Sequence 2, Appl
C 289	16	57.1	119801	4	US-09-949-016-13453	Sequence 13453, A	C 362	15.6	55.7	1150	4	US-09-620-314D-630	Sequence 630, App
C 290	16	57.1	137753	4	US-09-949-016-17404	Sequence 17404, A	C 363	15.6	55.7	1263	4	US-09-724-797-37	Sequence 37, Appl
C 291	16	57.1	161900	4	US-09-949-016-12685	Sequence 12685, A	C 364	15.6	55.7	1503	3	US-08-307-499-41	Sequence 41, Appl
C 292	16	57.1	161914	4	US-09-949-016-12906	Sequence 12906, A	C 365	15.6	55.7	1503	3	US-09-299-268-41	Sequence 41, Appl
C 293	16	57.1	162841	4	US-09-949-016-13733	Sequence 13733, A	C 366	15.6	55.7	1525	3	US-09-799-451-618	Sequence 618, App
C 294	16	57.1	169334	4	US-09-949-016-15999	Sequence 15999, A	C 367	15.6	55.7	1596	3	US-09-484-970B-148	Sequence 148, App
C 295	16	57.1	183112	4	US-09-949-016-15494	Sequence 15494, A	C 368	15.6	55.7	1910	3	US-09-221-017B-234	Sequence 234, App
C 296	16	57.1	183770	4	US-09-949-016-15494	Sequence 15494, A	C 369	15.6	55.7	1920	4	US-09-902-540-6398	Sequence 6398, App
C 297	16	57.1	193555	4	US-09-949-016-15553	Sequence 15553, A	C 370	15.6	55.7	1921	4	US-09-540-236-739	Sequence 739, App
C 298	16	57.1	193555	4	US-09-949-016-15555	Sequence 15554, A	C 371	15.6	55.7	2019	4	US-09-540-236-739	Sequence 739, App
C 299	16	57.1	193555	4	US-09-949-016-15555	Sequence 15555, A	C 372	15.6	55.7	2077	4	US-09-620-312D-985	Sequence 985, App
C 300	16	57.1	211049	4	US-09-949-016-15770	Sequence 15770, A	C 373	15.6	55.7	2257	4	US-09-808-701A-2	Sequence 2, Appl
C 301	16	57.1	422592	4	US-09-949-016-14182	Sequence 14182, A	C 374	15.6	55.7	3366	1	US-08-469-802B-1	Sequence 1, Appl
C 302	16	57.1	4403765	3	US-09-103-840A-1	Sequence 2, Appl	C 375	15.6	55.7	3366	1	US-08-267-803B-1	Sequence 1, Appl
C 303	16	57.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl	C 376	15.6	55.7	3602	3	US-09-402-929-1	Sequence 1, Appl
C 304	15.8	56.4	393	4	US-09-513-999C-2598	Sequence 2598, Ap	C 377	15.6	55.7	3699	4	US-09-248-796A-460	Sequence 460, App
C 305	15.8	56.4	453	4	US-09-621-976-1609	Sequence 1609, Ap	C 378	15.6	55.7	4880	3	US-09-402-929-5	Sequence 5, Appl
C 306	15.8	56.4	601	4	US-09-949-016-52932	Sequence 52932, A	C 379	15.6	55.7	5211	1	US-08-447-411-1	Sequence 1, Appl
C 307	15.8	56.4	601	4	US-09-949-016-15917	Sequence 15917, A	C 380	15.6	55.7	6775	3	US-09-402-929-4	Sequence 4, Appl
C 308	15.8	56.4	601	4	US-09-949-016-163712	Sequence 163712, A	C 381	15.6	55.7	8040	1	US-08-596-291-1	Sequence 1, Appl
C 309	15.8	56.4	601	4	US-09-949-016-169681	Sequence 169681, A	C 382	15.6	55.7	8040	1	US-09-100-804-1	Sequence 1, Appl
C 310	15.8	56.4	2310	4	US-09-543-681A-3003	Sequence 3003, Ap	C 383	15.6	55.7	8043	5	PCT-US94-09943-1	Sequence 1, Appl
C 311	15.8	56.4	2686	3	US-09-228-986-3	Sequence 3, Appl	C 384	15.6	55.7	8119	3	US-09-290-640-45	Sequence 45, Appl
C 312	15.8	56.4	2686	4	US-10-101-464A-3	Sequence 3, Appl	C 385	15.6	55.7	8119	3	US-09-665-615B-45	Sequence 45, Appl
C 313	15.8	56.4	13261	4	US-09-949-016-15645	Sequence 15645, A	C 386	15.6	55.7	8287	4	US-09-023-655-1441	Sequence 1441, Ap
C 314	15.8	56.4	14566	4	US-09-949-016-16765	Sequence 16765, A	C 387	15.6	55.7	13198	4	US-09-949-016-16425	Sequence 16425, A
C 315	15.8	56.4	19383	4	US-09-949-016-16031	Sequence 16031, A	C 388	15.6	55.7	14176	1	US-08-307-499-1	Sequence 1, Appl
C 316	15.8	56.4	21048	4	US-09-949-016-16091	Sequence 16091, A	C 389	15.6	55.7	14176	1	US-08-307-499-14	Sequence 14, Appl
C 317	15.8	56.4	27360	4	US-09-949-016-17502	Sequence 17502, A	C 390	15.6	55.7	14176	3	US-09-299-268-1	Sequence 1, Appl
C 318	15.8	56.4	35355	4	US-09-949-016-14197	Sequence 14197, A	C 391	15.6	55.7	14176	3	US-09-299-268-14	Sequence 14, Appl
C 319	15.8	56.4	42574	4	US-09-949-016-17525	Sequence 17525, A	C 392	15.6	55.7	15116	4	US-09-949-016-12354	Sequence 12354, A

C 393 15.6 55.7 15117 4 US-09-949-016-16260 Sequence 16260, A 466 15.6 55.7 390416 4 US-09-949-016-16923 Sequence 16923, A
C 394 15.6 55.7 22846 2 US-08-469-461-3 Sequence 3, Appli 467 15.4 55.0 212 4 US-09-513-999C-13969 Sequence 13969, A
C 395 15.6 55.7 22846 3 US-07-890-609-3 Sequence 3, Appli 468 15.4 55.0 226 4 US-09-513-999C-15683 Sequence 15683, A
C 396 15.6 55.7 23669 4 US-09-949-016-15296 Sequence 15296, A 469 15.4 55.0 264 4 US-09-248-796A-11073 Sequence 11073, A
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C 452 15.6 55.7 134987 4 US-09-949-016-15349 Sequence 15349, A
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C 461 15.6 55.7 176006 4 US-09-949-016-16804 Sequence 16804, A
C 462 15.6 55.7 192700 4 US-09-949-016-11820 Sequence 11820, A
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C 465 15.6 55.7 317366 4 US-09-949-016-16001 Sequence 16001, A

RESULT 1
US-08-869-423-1/c
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochel, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffmann, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cnd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:

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NAME: Kalish, Daniel
REGISTRATION NUMBER: 33,599
REFERENCE/DOCKET NUMBER: NC 77,654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-5642
TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: New Guinea C
POSITION IN GENOME:
CHROMOSOME/SEGMENT: PreM and Envelope
MAP POSITION: 330-2446
UNITS: bp
PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
AUTHORS: Woo, W S
AUTHORS: Biedrzycka, A
AUTHORS: Wright, P J
TITLE: Partial nucleotide sequence and deduced amino
TITLE: acid sequence of the structural proteins of dengue
TITLE: virus type 2, New Guinea C and PUO-218 strains
JOURNAL: J. Gen. Virol.
VOLUME: 69
PAGES: 1391-1398
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Irie, K
AUTHORS: Mohan, P M
AUTHORS: Sasaguri, Y
AUTHORS: Putnak, R
AUTHORS: Padmanabhan, R
TITLE: Sequence Analysis of Cloned dengue virus type
TITLE: 2 genome (New Guinea-C strain)
JOURNAL: Gene
VOLUME: 75
ISSUE: 2
PAGES: 197-211
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: Yaegashi, T
AUTHORS: Vakharia, V N
AUTHORS: Page, K
AUTHORS: Sasaguri, Y
AUTHORS: Feighny, R
AUTHORS: Padmanabhan, R
JOURNAL: Gene
VOLUME: 46
ISSUE: 2-3
PAGES: 257-267
DATE: 1986
US-08-937-195-1/c
Sequence 1, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVI, JOHN M.
APPLICANT: KAKANO, BILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
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LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
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LOCATION: 1218
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OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1260
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762
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OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1929
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Query Match 89.3%; Score 25; DB 3; Length 2357;
Best Local Similarity 89.3%; Pred. No. 0.07;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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, OTHER INFORMATION: /note= "Start of coding strand
, OTHER INFORMATION: sequence for NS1"
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, PUBLICATION INFORMATION:
, AUTHORS: Hahn, Y.S.
, JOURNAL: Virology
, VOLUME: 162
, PAGES: 167-180
, DATE: 1988
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, US-08-937-195-1
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, Query Match 77.9%, Score 21.8; DB 3; Length 3381;
, Best Local Similarity 82.1%; Pred. No. 2.3;
, Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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, Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181
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, RESULT 3
, US-08-937-195-2/c
, Sequence 2, Application US/08937195
, Patent No. 6136561
, GENERAL INFORMATION:
, APPLICANT: IVY, JOHN M.
, APPLICANT: KAKANO, EILEEN
, APPLICANT: CLEMENTS, DAVID
, TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
, NUMBER OF SEQUENCES: 18
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: MORRISON & FOERSTER
, STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
, CITY: WASHINGTON
, STATE: DC
, COUNTRY: USA
, ZIP: 20006-1812
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/937,195
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, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APLICATION NUMBER: US 08/488,807
, FILING DATE: 07-JUN-1995
, ATTORNEY/AGENT INFORMATION:
, NAME: MURASHIGE, KATE H.
, REGISTRATION NUMBER: 29,959
, REFERENCE/DOCKET NUMBER: 4733-0003.20
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (202) 887-1500
, TELEFAX: (202) 887-0763
, TELEX: 90-4030
, INFORMATION FOR SEQ ID NO: 2:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 3381 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
, ORIGINAL SOURCE:
, ORGANISM: Dengue virus
, STRAIN: Serotype 2(DEN-2)
, IMMEDIATE SOURCE:
, CLONE: Den-2 PR159/S1
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, LOCATION: 1216..1218
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, OTHER INFORMATION: /note= "GTG(coding for Val) is
, OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
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; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
US-08-937-195-2
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181

RESULT 4
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; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
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; CLONE: Den-2 PR159/S1
; FEATURE:
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; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain"
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
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; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
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; OTHER INFORMATION: sequence for Capsid."
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
US-08-915-152-1
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
Db 208 CCCATCTTTTAAATATCCCTGCTGTGG 181
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RESULT 5

US-08-915-152-2/c
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; replaced by GTT(coding for Val) for the wild-type DEN-2 PR159

; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-2
Query Match 77.9%; Score 21.8; DB 3; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 CCATCTCTCANNATCCCTGCTGTGG 28
||||| ||| |||||||||
Db 208 CCATCTTTTAATATCCCTGCTGTGG 181
RESULT 6
US-09-376-463-2/c
; Sequence 2, Application US/09376463
; Patent No. 6749857
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.20
; CURRENT APPLICATION NUMBER: US/09/376,463
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381


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; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-09-376-463-2

Query Match 77.9%; Score 21.8; DB 4; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
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Db 208 CCCATCTCTTTTAATATCCCTGCTGTGG 181

RESULT 7
PCT-US96-07627-1/c
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1260
; OTHER INFORMATION: /note= "T is replaced by G for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1929
; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-1

Query Match 77.9%; Score 21.8; DB 5; Length 3381;
Best Local Similarity 82.1%; Pred. No. 2.3;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
||||| | | | | | | | | | | | | | | | | | | | | |
Db 208 CCCATCTCTTTTAATATCCCTGCTGTGG 181

RESULT 8
PCT-US96-07627-2/c
; Sequence 2, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: /strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: /strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: /strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR15
; OTHER INFORMATION: /strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; PCT-US96-07627-2
;
; Query Match 77.9%; Score 21.8; DB 5; Length 3381;
; Best Local Similarity 82.1%; Pred. No. 2.3;
; Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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; Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
; Db 208 CCCATCTTTTAATATCCCTGCTGTGG 181
;
; RESULT 9
; US-08-325-426B-1/c
; Sequence 1, Application US/08325426B
; Patent No. 6017535
```

```
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
; US-08-325-426B-1
;
; Query Match 72.1%; Score 20.2; DB 3; Length 10718;
; Best Local Similarity 78.6%; Pred. No. 17;
; Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 1 CCCATCTCNCANNATCCCTGCTGTGG 28
; Db 288 CCCATCTAGCCAAATTCCTGCTGTGG 261
;
; RESULT 10
; US-07-807-043B-8
; Sequence 8, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,043B
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; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION DATA: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; US-07-807-043B-8

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGACGAATCCCTGCTGT 1921

RESULT 11
US-08-190-411A-1
; Sequence 1, Application US/08190411A
; Patent No. 5541104
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,411A
; FILING DATE: 01-FEBRUARY-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION DATA: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5541104man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; US-08-190-411A-1

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGACGAATCCCTGCTGT 1921

RESULT 12
US-08-299-849B-8
; Sequence 8, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szkora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; APPLICATION NUMBER: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5612201man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5355
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5674 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: genomic DNA
;; FEATURE:
;; NAME/KEY: MAGE-1 gene
US-08-299-849B-8

Query Match 67.1%; Score 18.8; DB 1; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 13
US-08-560-024-1
; Sequence 1, Application US/08560024
; Patent No. 5843448
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsung; Stockert, Elisabeth;
; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,024
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,411
; FILING DATE: 01-FEBRUARY-1994
; APPLICATION NUMBER: 037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/807,043
;; FILING DATE: 12-DECEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; APPLICATION NUMBER: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5843448man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5354
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5674 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: genomic DNA
;; FEATURE:
;; NAME/KEY: MAGE-1 gene
US-08-560-024-1

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 14
US-08-142-368A-8
; Sequence 8, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5925729man D.
; REGISTRATION NUMBER: 30,946
; APPLICATION NUMBER: LUD 5253.4-US
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 688-9200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-142-368A-8

Query Match 67.1%; Score 18.8; DB 2; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 15
US-08-967-727-8
; Sequence 8, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-967-727-8

Query Match 67.1%; Score 18.8; DB 3; Length 5674;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCNCANNATCCCTGCTGT 25
Db 1897 CTCATCTTGTGAGATCCCTGCTGT 1921

RESULT 16
US-08-037-230D-8
; Sequence 8, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6235525man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353

QY 1 CCCATCTCCTCANNATCCCTGCTGT 25

Query Match	66.4%;	Score 18.6;	DB 4;	Length 767677;
Best Local Similarity	75.0%;	Pred. No. 2.4e+02;		
Matches	21;	Conservative	0;	Mismatches 7; Indels 0;
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RESULT 27
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOW
; TITLE OF INVENTION: WITH HUMAN DISEASE, I
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

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LOCATION: (1) ... (767677)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-17361

Query Match 66.4%; Score 18.6; DB 4; Length 767677;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTTGG 28
DB 366317 CCCACCTCTCCCATCCCTGCTGTTGG 366290

RESULT 28
US-09-949-016-108599
; Sequence 108599, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108599
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-108599

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 70;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTT 26
DB 440 CCCCTCTCTCAGTCTCTCTGCTGTT 465

RESULT 29
US-09-949-016-2987/c
; Sequence 2987, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2987
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2987

Query Match 65.0%; Score 18.2; DB 4; Length 2290;
Best Local Similarity 76.9%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTT 26

DB 1464 CCCCTCTCTCAGTCTCTCTGCTGTT 1439

RESULT 30
US-08-437-607A-3/c
; Sequence 3, Application US/08437607A
; Patent No. 555579
; GENERAL INFORMATION:
; APPLICANT: Leonard, James N. Montminy, Marc R.
; TITLE OF INVENTION: ISLET-SPECIFIC HOMEOPROTEIN AND TRANSCRIPTIONAL
; REGULATOR OF INSULIN GENE EXPRESSION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,607A
; FILING DATE: MAY 9, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1110-1-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2917 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Human HoxB13 gene
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 582..1184
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1185..2132
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2133..2384
US-08-437-607A-3

Query Match 65.0%; Score 18.2; DB 2; Length 2917;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTT 26
DB 2859 CCCCTCTCTCAGTCTCTCTGCTGTT 2834

RESULT 31
US-09-439-313-333/c
; Sequence 333, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

RESULT 37
US-09-679-426-333/c
; Sequence 333, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: DILLON, DAVIN C.

Query Match 65.0%; Score 18.2; DB 4; Length 3030;

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Best Local Similarity 76.9%; Pred. No. 1e+02; Mismatches 6; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 CCCATCTCCTCAGTCCTCTCTGCTGTT 26
Db 1455 CCCCTCTCCTCAGTCCTCTCTGCTGTT 1430

RESULT 39
US-09-651-236-333/c
; Sequence 333, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-333

Query Match 65.0%; Score 18.2; DB 4; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCCTCTCTGCTGTT 26
Db 1455 CCCCTCTCCTCAGTCCTCTCTGCTGTT 1430

RESULT 40
US-09-949-016-14729/c
; Sequence 14729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14729
; LENGTH: 7242
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14729

Query Match 65.0%; Score 18.2; DB 4; Length 7242;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCCTCTCTGCTGTT 26
Db 4415 CCCCTCTCCTCAGTCCTCTCTGCTGTT 4390
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GenCore version 5.1.6
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Title: US-10-085-944-1

Perfect score: 28

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	25	89.3	10649	21	US-10-719-547-14
C 4	25	89.3	10649	21	US-10-719-547-16
C 5	25	89.3	10724	19	US-10-699-550-4
C 6	21.8	77.9	3381	16	US-10-247-960-2
C 7	21.8	77.9	15159	21	US-10-871-775-30
Sequence 1, Appli					
Sequence 18, Appli					
Sequence 14, Appli					
Sequence 16, Appli					
Sequence 4, Appli					
Sequence 2, Appli					
Sequence 30, Appli					

C 8	20.2	72.1	10735	19	US-10-699-550-3	Sequence 3, Appli
C 9	19.2	68.6	422	20	US-10-425-115-162694	Sequence 162694,
C 10	19.2	68.6	691	13	US-10-027-632-281617	Sequence 281617,
C 11	19.2	68.6	691	17	US-10-027-632-281617	Sequence 281617,
C 12	19.2	68.6	52746	22	US-10-737-082-39	Sequence 39, Appli
C 13	19.2	68.6	52746	22	US-10-765-790-39	Sequence 39, Appli
C 14	18.8	67.1	2739	19	US-10-437-963-62174	Sequence 62174, A
C 15	18.6	66.4	482	16	US-10-029-386-27304	Sequence 27304, A
C 16	18.6	66.4	486	9	US-09-864-761-27448	Sequence 27448, A
C 17	18.6	66.4	577	16	US-10-029-386-13604	Sequence 13604, A
C 18	18.6	66.4	2301	19	US-10-437-963-53513	Sequence 53513, A
C 19	18.6	66.4	6412	19	US-10-322-281-484	Sequence 484, A
C 20	18.6	66.4	61396	19	US-10-322-281-484	Sequence 483, App
C 21	18.6	66.4	98634	13	US-10-087-192-1870	Sequence 1870, Ap
C 22	18.2	65.0	476	10	US-09-814-353-1708	Sequence 1708, Ap
C 23	18.2	65.0	476	10	US-09-814-353-8061	Sequence 8061, Ap
C 24	18.2	65.0	1506	13	US-10-027-632-256653	Sequence 256653,
C 25	18.2	65.0	1506	17	US-10-027-632-256653	Sequence 256653,
C 26	18.2	65.0	1928	20	US-10-357-930-30260	Sequence 30260, A
C 27	18.2	65.0	2385	21	US-10-918-897-12	Sequence 12, Appli
C 28	18.2	65.0	3030	9	US-09-759-143-333	Sequence 333, App
C 29	18.2	65.0	3030	9	US-09-780-669-333	Sequence 333, App
C 30	18.2	65.0	3030	9	US-09-822-827-333	Sequence 333, App
C 31	18.2	65.0	3030	9	US-09-232-880-333	Sequence 333, App
C 32	18.2	65.0	3030	9	US-09-895-793-333	Sequence 333, App
C 33	18.2	65.0	3030	9	US-09-895-814-333	Sequence 333, App
C 34	18.2	65.0	3030	13	US-10-012-896-333	Sequence 333, App
C 35	18.2	65.0	3030	14	US-10-010-940-333	Sequence 333, App
C 36	18.2	65.0	3030	16	US-10-144-678A-333	Sequence 333, App
C 37	18.2	65.0	3030	16	US-10-294-025-333	Sequence 333, App
C 38	18.2	65.0	77777	19	US-10-318-389-4	Sequence 4, Appli
C 39	18.2	65.0	81826	14	US-10-175-523-197	Sequence 197, App
C 40	18.2	65.0	117985	20	US-10-719-993-7053	Sequence 7053, Ap
C 41	17.8	63.6	415	13	US-10-027-632-183225	Sequence 183225,
C 42	17.8	63.6	415	17	US-10-027-632-183225	Sequence 183225,
C 43	17.8	63.6	599	22	US-10-972-079-6916	Sequence 6916, Ap
C 44	17.8	63.6	600	22	US-10-972-079-25350	Sequence 25350, A
C 45	17.8	63.6	600	22	US-10-972-079-25351	Sequence 25351, A
C 46	17.8	63.6	600	22	US-10-972-079-25352	Sequence 25352, A
C 47	17.8	63.6	713	19	US-10-767-701-7611	Sequence 7611, Ap
C 48	17.8	63.6	1277	19	US-10-437-963-83170	Sequence 83170, A
C 49	17.8	63.6	90798	19	US-10-318-819A-4	Sequence 4, Appli
C 50	17.6	62.9	239	9	US-09-864-761-26181	Sequence 26181, A
C 51	17.6	62.9	240	20	US-10-425-115-179950	Sequence 179950,
C 52	17.6	62.9	353	11	US-09-864-408A-2719	Sequence 2719, Ap
C 53	17.6	62.9	371	19	US-10-437-963-13942	Sequence 13942, A
C 54	17.6	62.9	410	9	US-09-864-761-21296	Sequence 21296, A
C 55	17.6	62.9	453	10	US-09-918-995-14536	Sequence 14536, A
C 56	17.6	62.9	494	9	US-09-864-761-4549	Sequence 4549, Ap
C 57	17.6	62.9	566	9	US-09-864-761-9825	Sequence 9825, Ap
C 58	17.6	62.9	599	22	US-10-972-079-66362	Sequence 66362, A
C 59	17.6	62.9	599	22	US-10-972-079-66363	Sequence 66363, A
C 60	17.6	62.9	600	22	US-10-972-079-71643	Sequence 71643, A
C 61	17.6	62.9	649	13	US-10-027-632-275006	Sequence 275006,
C 62	17.6	62.9	749	17	US-10-027-632-275006	Sequence 275006,
C 63	17.6	62.9	700	17	US-10-341-961A-7	Sequence 7, Appli
C 64	17.6	62.9	796	13	US-10-027-632-156282	Sequence 156282,
C 65	17.6	62.9	796	17	US-10-027-632-156282	Sequence 156282,
C 66	17.6	62.9	858	18	US-10-424-599-106253	Sequence 106253,
C 67	17.6	62.9	905	13	US-10-027-632-160675	Sequence 160675,
C 68	17.6	62.9	905	13	US-10-027-632-160675	Sequence 160675,
C 69	17.6	62.9	905	17	US-10-027-632-160675	Sequence 160675,
C 70	17.6	62.9	905	17	US-10-027-632-160676	Sequence 160676,
C 71	17.6	62.9	939	21	US-10-774-355A-123	Sequence 123, App
C 72	17.6	62.9	945	17	US-10-387-629-163	Sequence 163, App
C 73	17.6	62.9	945	18	US-10-343-650A-159	Sequence 159, App
C 74	17.6	62.9	949	13	US-10-027-632-256985	Sequence 256985,
C 75	17.6	62.9	949	13	US-10-027-632-256986	Sequence 256986,
C 76	17.6	62.9	949	17	US-10-027-632-256985	Sequence 256985,
C 77	17.6	62.9	949	17	US-10-027-632-256986	Sequence 256986,
C 78	17.6	62.9	982	10	US-09-844-861A-21	Sequence 21, Appli
C 79	17.6	62.9	1092	10	US-09-814-353-21323	Sequence 21323, A
C 80	17.6	62.9	1151	10	US-09-844-861A-19	Sequence 19, Appli

81	17.6	62.9	1345	15	US-10-017-161-877	Sequence 877, App	c 154	17.2	61.4	6752	15	US-10-084-817-34	Sequence 34, Appl
82	17.6	62.9	1345	17	US-10-292-798-755	Sequence 855, App	c 155	17.2	61.4	6754	15	US-10-101-510-534	Sequence 534, App
83	17.6	62.9	1400	9	US-09-886-055-86	Sequence 76, Appl	c 156	17.2	61.4	6964	10	US-09-816-653A-5	GENERAL INFORMATI
84	17.6	62.9	1400	10	US-09-804-291-86	Sequence 86, Appl	c 157	17.2	61.4	19868	19	US-10-315-962-4	Sequence 4, Appl1
85	17.6	62.9	1514	9	US-09-738-546-1	Sequence 1, Appl1	c 158	17.2	61.4	23587	10	US-09-764-891-9788	Sequence 9788, App
86	17.6	62.9	1514	11	US-09-836-544-7	Sequence 7, Appl1	c 159	17.2	61.4	59394	11	US-09-997-722-235	Sequence 235, App
87	17.6	62.9	1514	15	US-10-207-655-98	Sequence 98, Appl	c 160	17.2	61.4	160921	13	US-10-087-192-1672	Sequence 1672, App
88	17.6	62.9	1514	18	US-10-641-643-1316	Sequence 1316, App	c 161	17.2	61.4	171936	15	US-10-265-071-24	Sequence 24, Appl
89	17.6	62.9	1514	21	US-10-802-440-11	Sequence 11, Appl	c 162	17.2	61.4	171936	17	US-10-025-966A-24	Sequence 24, Appl
90	17.6	62.9	1514	21	US-10-616-865-11	Sequence 11, Appl	c 163	17.2	61.4	231000	17	US-10-174-014-12	Sequence 12, Appl
91	17.6	62.9	1514	24	US-11-027-053-11	Sequence 11, Appl	c 164	17.2	61.4	233380	13	US-10-087-192-652	Sequence 652, App
92	17.6	62.9	2170	9	US-09-925-300-642	Sequence 642, App	c 165	17.2	61.4	338702	13	US-10-087-192-292	Sequence 292, App
93	17.6	62.9	3803	16	US-10-076-934-1	Sequence 1, Appl1	c 166	17.2	61.4	439892	13	US-10-087-192-454	Sequence 454, App
94	17.6	62.9	3804	11	US-09-997-722-257	Sequence 257, App	c 167	17.2	60.7	121	10	US-09-818-875-1844	Sequence 1844, App
95	17.6	62.9	3804	16	US-10-143-238-1	Sequence 1, Appl1	c 168	17.2	60.7	121	10	US-09-818-875-1845	Sequence 1845, App
96	17.6	62.9	3806	10	US-09-835-297-3	Sequence 3, Appl1	c 169	17.2	60.7	121	10	US-09-818-875-1848	Sequence 1848, App
97	17.6	62.9	4740	19	US-10-437-963-51241	Sequence 51241, A	c 170	17.2	60.7	121	10	US-09-818-875-1849	Sequence 1849, App
98	17.6	62.9	19025	14	US-10-274-878-3	Sequence 3, Appl1	c 171	17.2	60.7	121	10	US-09-818-875-1852	Sequence 1852, App
99	17.6	62.9	19025	18	US-10-697-266-3	Sequence 3, Appl1	c 172	17.2	60.7	121	10	US-09-818-875-1853	Sequence 1853, App
100	17.6	62.9	31960	14	US-10-114-170-11	Sequence 11, Appl	c 173	17.2	60.7	121	10	US-09-818-875-1856	Sequence 1856, App
101	17.6	62.9	51365	11	US-09-997-722-256	Sequence 256, App	c 174	17.2	60.7	121	10	US-09-818-875-1857	Sequence 1857, App
102	17.6	62.9	133760	18	US-10-240-425-1101	Sequence 1101, App	c 175	17.2	60.7	121	10	US-09-818-875-1860	Sequence 1860, App
103	17.6	62.9	177587	13	US-10-087-192-1438	Sequence 1438, App	c 176	17.2	60.7	121	10	US-09-818-875-1861	Sequence 1861, App
104	17.6	62.9	321491	13	US-10-087-192-532	Sequence 532, App	c 177	17.2	60.7	121	10	US-09-818-875-1864	Sequence 1864, App
105	17.6	62.9	340449	11	US-09-903-582-3	Sequence 3, Appl1	c 178	17.2	60.7	121	10	US-09-818-875-1865	Sequence 1865, App
106	17.4	62.1	345	11	US-09-732-627A-1005	Sequence 1005, App	c 179	17.2	60.7	121	10	US-09-818-875-1868	Sequence 1868, App
107	17.4	62.1	486	20	US-10-425-115-180032	Sequence 180032, App	c 180	17.2	60.7	121	10	US-09-818-875-1869	Sequence 1869, App
108	17.4	62.1	872	13	US-10-027-632-164829	Sequence 164829, App	c 181	17.2	60.7	121	10	US-09-818-875-1872	Sequence 1872, App
109	17.4	62.1	872	17	US-10-027-632-164829	Sequence 164829, App	c 182	17.2	60.7	121	10	US-09-818-875-1873	Sequence 1873, App
110	17.4	62.1	41637	11	US-09-997-722-103	Sequence 103, App	c 183	17.2	60.7	121	10	US-09-818-875-1876	Sequence 1876, App
111	17.4	62.1	88191	9	US-09-799-799-3	Sequence 3, Appl1	c 184	17.2	60.7	121	17	US-10-209-787-1877	Sequence 1877, App
112	17.2	61.4	259	17	US-10-242-535A-25273	Sequence 25273, A	c 185	17.2	60.7	121	17	US-10-209-787-1844	Sequence 1844, App
113	17.2	61.4	259	18	US-10-085-783A-25273	Sequence 25273, A	c 186	17.2	60.7	121	17	US-10-209-787-1845	Sequence 1845, App
114	17.2	61.4	463	18	US-10-344-928-18	Sequence 18, Appl	c 187	17.2	60.7	121	17	US-10-209-787-1848	Sequence 1848, App
115	17.2	61.4	515	13	US-10-027-632-38038	Sequence 38038, A	c 188	17.2	60.7	121	17	US-10-209-787-1849	Sequence 1849, App
116	17.2	61.4	515	13	US-10-027-632-38038	Sequence 38038, A	c 189	17.2	60.7	121	17	US-10-209-787-1852	Sequence 1852, App
117	17.2	61.4	527	13	US-10-027-632-182494	Sequence 182494, A	c 190	17.2	60.7	121	17	US-10-209-787-1853	Sequence 1853, App
118	17.2	61.4	527	17	US-10-027-632-182494	Sequence 182494, A	c 191	17.2	60.7	121	17	US-10-209-787-1856	Sequence 1856, App
119	17.2	61.4	527	13	US-10-027-632-255432	Sequence 255432, A	c 192	17.2	60.7	121	17	US-10-209-787-1857	Sequence 1857, App
120	17.2	61.4	652	13	US-10-027-632-255433	Sequence 255433, A	c 193	17.2	60.7	121	17	US-10-209-787-1860	Sequence 1860, App
121	17.2	61.4	652	13	US-10-027-632-255434	Sequence 255434, A	c 194	17.2	60.7	121	17	US-10-209-787-1861	Sequence 1861, App
122	17.2	61.4	652	17	US-10-027-632-255432	Sequence 255432, A	c 195	17.2	60.7	121	17	US-10-209-787-1864	Sequence 1864, App
123	17.2	61.4	652	17	US-10-027-632-255433	Sequence 255433, A	c 196	17.2	60.7	121	17	US-10-209-787-1865	Sequence 1865, App
124	17.2	61.4	652	17	US-10-027-632-255434	Sequence 255434, A	c 197	17.2	60.7	121	17	US-10-209-787-1868	Sequence 1868, App
125	17.2	61.4	713	13	US-10-027-632-18382	Sequence 18382, A	c 198	17.2	60.7	121	17	US-10-209-787-1869	Sequence 1869, App
126	17.2	61.4	713	17	US-10-027-632-18382	Sequence 18382, A	c 199	17.2	60.7	121	17	US-10-209-787-1872	Sequence 1872, App
127	17.2	61.4	727	19	US-10-437-963-4633	Sequence 4633, App	c 200	17.2	60.7	121	17	US-10-209-787-1873	Sequence 1873, App
128	17.2	61.4	785	13	US-10-027-632-148435	Sequence 148435, App	c 201	17.2	60.7	121	17	US-10-209-787-1876	Sequence 1876, App
129	17.2	61.4	785	17	US-10-027-632-148435	Sequence 148435, App	c 202	17.2	60.7	121	17	US-10-209-787-1877	Sequence 1877, App
130	17.2	61.4	1023	15	US-10-437-963-6252	Sequence 6252, App	c 203	17.2	60.7	121	17	US-10-261-185-1845	Sequence 1845, App
131	17.2	61.4	1334	15	US-10-101-510-505	Sequence 505, App	c 204	17.2	60.7	121	17	US-10-261-185-1845	Sequence 1845, App
132	17.2	61.4	1349	18	US-10-424-599-130164	Sequence 130164, App	c 205	17.2	60.7	121	17	US-10-261-185-1848	Sequence 1848, App
133	17.2	61.4	1353	14	US-10-453-668-267	Sequence 267, App	c 206	17.2	60.7	121	17	US-10-261-185-1849	Sequence 1849, App
134	17.2	61.4	1519	17	US-10-341-434-179	Sequence 179, App	c 207	17.2	60.7	121	17	US-10-261-185-1852	Sequence 1852, App
135	17.2	61.4	1519	19	US-10-693-999-22	Sequence 22, Appl	c 208	17.2	60.7	121	17	US-10-261-185-1853	Sequence 1853, App
136	17.2	61.4	1581	19	US-10-437-963-62172	Sequence 62172, A	c 209	17.2	60.7	121	17	US-10-261-185-1856	Sequence 1856, App
137	17.2	61.4	1638	17	US-10-369-493-45046	Sequence 45046, A	c 210	17.2	60.7	121	17	US-10-261-185-1857	Sequence 1857, App
138	17.2	61.4	1927	14	US-10-453-668-379	Sequence 379, App	c 211	17.2	60.7	121	17	US-10-261-185-1860	Sequence 1860, App
139	17.2	61.4	1927	14	US-10-453-668-381	Sequence 381, App	c 212	17.2	60.7	121	17	US-10-261-185-1861	Sequence 1861, App
140	17.2	61.4	2154	19	US-10-437-963-12481	Sequence 12481, A	c 213	17.2	60.7	121	17	US-10-261-185-1864	Sequence 1864, App
141	17.2	61.4	3294	19	US-10-437-963-62175	Sequence 62175, A	c 214	17.2	60.7	121	17	US-10-261-185-1865	Sequence 1865, App
142	17.2	61.4	4090	19	US-10-437-963-51235	Sequence 51235, A	c 215	17.2	60.7	121	17	US-10-261-185-1868	Sequence 1868, App
143	17.2	61.4	4119	10	US-09-764-891-6600	Sequence 6600, App	c 216	17.2	60.7	121	17	US-10-261-185-1869	Sequence 1869, App
144	17.2	61.4	4119	14	US-10-091-572-464	Sequence 464, App	c 217	17.2	60.7	121	17	US-10-261-185-1872	Sequence 1872, App
145	17.2	61.4	4124	10	US-09-764-891-6599	Sequence 6599, App	c 218	17.2	60.7	121	17	US-10-261-185-1873	Sequence 1873, App
146	17.2	61.4	4124	14	US-10-091-572-463	Sequence 463, App	c 219	17.2	60.7	121	17	US-10-261-185-1876	Sequence 1876, App
147	17.2	61.4	5358	19	US-10-437-963-24917	Sequence 24917, A	c 220	17.2	60.7	121	17	US-10-261-185-1877	Sequence 1877, App
148	17.2	61.4	5781	15	US-10-299-058-1	Sequence 1, Appl1	c 221	17.2	60.7	121	19	US-10-681-074-1844	Sequence 1844, App
149	17.2	61.4	5781	15	US-10-299-058-3	Sequence 3, Appl1	c 222	17.2	60.7	121	19	US-10-681-074-1845	Sequence 1845, App
150	17.2	61.4	6204	9	US-09-880-107-3036	Sequence 3036, App	c 223	17.2	60.7	121	19	US-10-681-074-1848	Sequence 1848, App
151	17.2	61.4	6204	10	US-10-372-683-3	Sequence 3, Appl1	c 224	17.2	60.7	121	19	US-10-681-074-1849	Sequence 1849, App
152	17.2	61.4	6297	21	US-10-956-157-820	Sequence 820, App	c 225	17.2	60.7	121	19	US-10-681-074-1852	Sequence 1852, App
153	17.2	61.4	6482	18	US-10-363-616-212	Sequence 212, App	c 226	17.2	60.7	121	19	US-10-681-074-1853	Sequence 1853, App

227	17	60.7	121	19	US-10-681-074-1856	Sequence 1856, Ap	c 300	17	60.7	807	17	US-10-369-493-45415	Sequence 45415, A
c 228	17	60.7	121	19	US-10-681-074-1857	Sequence 1857, Ap	c 301	17	60.7	860	17	US-10-767-701-12334	Sequence 12334, A
229	17	60.7	121	19	US-10-681-074-1860	Sequence 1860, Ap	c 302	17	60.7	868	13	US-10-027-632-138164	Sequence 138164, A
c 230	17	60.7	121	19	US-10-681-074-1861	Sequence 1861, Ap	c 303	17	60.7	868	13	US-10-027-632-138165	Sequence 138165, A
231	17	60.7	121	19	US-10-681-074-1864	Sequence 1864, Ap	c 304	17	60.7	868	17	US-10-027-632-138164	Sequence 138164, A
c 232	17	60.7	121	19	US-10-681-074-1865	Sequence 1865, Ap	c 305	17	60.7	868	17	US-10-027-632-138165	Sequence 138165, A
233	17	60.7	121	19	US-10-681-074-1868	Sequence 1868, Ap	c 306	17	60.7	1125	19	US-10-437-963-10123	Sequence 10123, A
c 234	17	60.7	121	19	US-10-681-074-1869	Sequence 1869, Ap	c 307	17	60.7	1422	15	US-10-081-872-163	Sequence 163, App
235	17	60.7	121	19	US-10-681-074-1872	Sequence 1872, Ap	c 308	17	60.7	1422	17	US-10-385-305-163	Sequence 163, App
c 236	17	60.7	121	19	US-10-681-074-1873	Sequence 1873, Ap	c 309	17	60.7	1422	19	US-10-437-963-90255	Sequence 90255, A
237	17	60.7	121	19	US-10-681-074-1876	Sequence 1876, Ap	c 310	17	60.7	1893	19	US-10-437-963-20390	Sequence 20390, A
c 238	17	60.7	121	19	US-10-681-074-1877	Sequence 1877, Ap	c 311	17	60.7	2000	17	US-10-260-238-2159	Sequence 2159, Ap
239	17	60.7	201	20	US-10-719-993-8083	Sequence 8083, Ap	c 312	17	60.7	2163	19	US-10-437-963-39821	Sequence 39821, A
c 240	17	60.7	201	20	US-10-719-993-8679	Sequence 8679, Ap	c 313	17	60.7	2218	19	US-10-437-963-41458	Sequence 41458, A
241	17	60.7	201	21	US-10-741-600-6107	Sequence 6107, Ap	c 314	17	60.7	4371	21	US-10-813-507-12	Sequence 12, Appl
242	17	60.7	201	21	US-10-741-600-6108	Sequence 6108, Ap	c 315	17	60.7	4629	9	US-09-150-811-7	GENERAL INFORMA
243	17	60.7	201	21	US-10-741-600-6113	Sequence 6113, Ap	c 316	17	60.7	4999	13	US-09-740-211-14	Sequence 14, Appl
244	17	60.7	201	21	US-10-741-600-6184	Sequence 6184, Ap	c 317	17	60.7	4999	14	US-10-007-968-14	Sequence 14, Appl
245	17	60.7	201	21	US-10-741-600-6214	Sequence 6214, Ap	c 318	17	60.7	4999	17	US-10-293-400-14	Sequence 14, Appl
246	17	60.7	201	21	US-10-741-600-6234	Sequence 6234, Ap	c 319	17	60.7	6996	17	US-10-239-498A-1	Sequence 1, Appl
247	17	60.7	201	21	US-10-741-600-6236	Sequence 6236, Ap	c 320	17	60.7	6996	21	US-10-813-507-7	Sequence 7, Appl
248	17	60.7	201	21	US-10-741-600-6239	Sequence 6239, Ap	c 321	17	60.7	7931	18	US-10-411-037-29	Sequence 29, Appl
249	17	60.7	201	21	US-10-741-600-6240	Sequence 6240, Ap	c 322	17	60.7	7931	18	US-10-411-026-29	Sequence 29, Appl
250	17	60.7	201	21	US-10-741-600-6241	Sequence 6241, Ap	c 323	17	60.7	7931	18	US-10-410-962-29	Sequence 29, Appl
251	17	60.7	201	21	US-10-741-600-6242	Sequence 6242, Ap	c 324	17	60.7	7931	18	US-10-411-049-29	Sequence 29, Appl
252	17	60.7	201	21	US-10-741-600-6247	Sequence 6247, Ap	c 325	17	60.7	7931	18	US-10-410-930-29	Sequence 29, Appl
253	17	60.7	201	21	US-10-741-600-6253	Sequence 6253, Ap	c 326	17	60.7	7931	19	US-10-410-997-29	Sequence 29, Appl
254	17	60.7	201	21	US-10-741-600-6254	Sequence 6254, Ap	c 327	17	60.7	7931	19	US-10-411-012-29	Sequence 29, Appl
255	17	60.7	201	21	US-10-741-600-6256	Sequence 6256, Ap	c 328	17	60.7	7931	19	US-10-287-994-29	Sequence 29, Appl
256	17	60.7	201	21	US-10-741-600-6508	Sequence 6508, Ap	c 329	17	60.7	7931	21	US-10-410-913-29	Sequence 29, Appl
257	17	60.7	201	21	US-10-741-600-6509	Sequence 6509, Ap	c 330	17	60.7	7931	21	US-10-410-980-29	Sequence 29, Appl
258	17	60.7	201	21	US-10-741-600-6514	Sequence 6514, Ap	c 331	17	60.7	7931	21	US-10-410-897-29	Sequence 29, Appl
259	17	60.7	201	21	US-10-741-600-6585	Sequence 6585, Ap	c 332	17	60.7	7931	21	US-10-492-261-29	Sequence 29, Appl
260	17	60.7	201	21	US-10-741-600-6615	Sequence 6615, Ap	c 333	17	60.7	7944	13	US-10-095-718-1	Sequence 1, Appl
261	17	60.7	201	21	US-10-741-600-6635	Sequence 6635, Ap	c 334	17	60.7	7944	18	US-10-681-970-1	Sequence 1, Appl
262	17	60.7	201	21	US-10-741-600-6637	Sequence 6637, Ap	c 335	17	60.7	8720	17	US-10-239-498A-3	Sequence 3, Appl
263	17	60.7	201	21	US-10-741-600-6640	Sequence 6640, Ap	c 336	17	60.7	8967	20	US-10-472-516-1	Sequence 1, Appl
264	17	60.7	201	21	US-10-741-600-6641	Sequence 6641, Ap	c 337	17	60.7	8967	20	US-10-968-286-1	Sequence 1, Appl
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269	17	60.7	201	21	US-10-741-600-6655	Sequence 6655, Ap	c 342	17	60.7	9009	20	US-10-491-464-1	Sequence 1, Appl
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C 443	16.6	59.3	600	22	US-10-972-079-22442	Sequence 22442, A							
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ALIGNMENTS

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; Publication No. US202020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2

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US-10-085-944-1

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; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/719,547
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
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; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT FILING DATE: 2003-11-21
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US-10-085-944-1

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; Publication No. US20050010043A1
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; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
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US-10-719-547-16

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; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US/10/699,550
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
```

; PRIOR APPLICATION NUMBER: 60/281,947
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/275,025
 ; PRIOR FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 4
 ; LENGTH: 10724
 ; TYPE: DNA
 ; ORGANISM: Dengue virus type 2
 ; US-10-699-550-4

Query Match 89.3%; Score 25; DB 19; Length 10724;
 Best Local Similarity 89.3%; Pred. No. 0.12;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 Db 304 CCCATCTCTCAGTATCCCTGCTGTGG 277

RESULT 6

US-10-247-960-2/c
 ; Sequence 2, Application US/10247960
 ; Publication No. US20030175304A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hawaii Biotechnology Group, Inc.
 ; APPLICANT: Peters, Iain
 ; APPLICANT: Collier, Beth-Ann
 ; APPLICANT: McDonnell, Michael
 ; APPLICANT: Ivy, John
 ; APPLICANT: Harada, Kent
 ; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
 ; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
 ; FILE REFERENCE: 24733-20005.01
 ; CURRENT APPLICATION NUMBER: US/10/247,960
 ; CURRENT FILING DATE: 2002-12-17
 ; PRIOR APPLICATION NUMBER: 09/376,463
 ; PRIOR FILING DATE: 1999-08-16
 ; PRIOR APPLICATION NUMBER: 08/904,227
 ; PRIOR FILING DATE: 1997-07-31
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 3381
 ; TYPE: DNA
 ; ORGANISM: Dengue virus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(3381)
 ; US-10-247-960-2

Query Match 77.9%; Score 21.8; DB 16; Length 3381;
 Best Local Similarity 82.1%; Pred. No. 3.4;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 Db 208 CCCATCTCTTAAATATCCCTGCTGTGG 181

RESULT 7

US-10-871-775-30/c
 ; Sequence 30, Application US/10871775
 ; Publication No. US20050100886A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pletnev, Alexander
 ; APPLICANT: Putnak, Joseph Robert
 ; APPLICANT: Chanock, Robert M.
 ; APPLICANT: Murphy, Brian R.
 ; APPLICANT: Whitehead, Stephen S.
 ; APPLICANT: Blaney, Joseph E., Jr.
 ; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND

; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
 ; TITLE OF INVENTION: PREVENT DISEASE CAUSED BY WEST NILE VIRUS.
 ; FILE REFERENCE: NIH225.001C1
 ; CURRENT APPLICATION NUMBER: US/10/871,775
 ; CURRENT FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: PCT/US03/00594
 ; PRIOR FILING DATE: 2003-01-09
 ; PRIOR APPLICATION NUMBER: US 60/347,281
 ; PRIOR FILING DATE: 2002-01-10
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 15159
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Dengue2 (Tonga/74) plasmid p2
 ; US-10-871-775-30

Query Match 77.9%; Score 21.8; DB 21; Length 15159;
 Best Local Similarity 82.1%; Pred. No. 3.9;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 Db 304 CCCATCTCTTAAATATCCCTGCTGTGG 277

RESULT 8

US-10-699-550-3/c
 ; Sequence 3, Application US/10699550
 ; Publication No. US20040197769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WONG, SUSAN J.
 ; APPLICANT: SHI, PEI-YONG
 ; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
 ; FILE REFERENCE: 454311-2232.1
 ; CURRENT APPLICATION NUMBER: US/10/699,550
 ; CURRENT FILING DATE: 2003-10-31
 ; PRIOR APPLICATION NUMBER: 60/476,513
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 60/422,755
 ; PRIOR FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: PCT/US02/09036
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: 60/402,860
 ; PRIOR FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: 60/281,947
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/275,025
 ; PRIOR FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 3
 ; LENGTH: 10735
 ; TYPE: DNA
 ; ORGANISM: Dengue virus type 1
 ; US-10-699-550-3

Query Match 72.1%; Score 20.2; DB 19; Length 10735;
 Best Local Similarity 78.6%; Pred. No. 22;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCTCANNATCCCTGCTGTGG 28
 Db 302 CCCATCTAGCCAAAATTCCTGCTGTGG 275

RESULT 9

US-10-425-115-162694/c
 ; Sequence 162694, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:

```
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 162694
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_79953C.1
US-10-425-115-162694

Query Match      68.6%; Score 19.2; DB 20; Length 422;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 CCATCTCCTCANNATCCCTGCTGTGG 28
Db      338 CCATCTCCGAGGTTCCCTGCTGTGG 312

RESULT 10
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match      68.6%; Score 19.2; DB 13; Length 691;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 CCCATCTCCTCANNATCCCTGCTGTGG 27
Db      562 CCCAGCTCCTCATGTTCCCTGCTGTGG 536

RESULT 11
US-10-027-632-281617/c
; Sequence 281617, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281617
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281617

Query Match      68.6%; Score 19.2; DB 22; Length 52746;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 CCCATCTCCTCANNATCCCTGCTGTGG 27
Db      562 CCCAGCTCCTCATGTTCCCTGCTGTGG 536

RESULT 12
US-10-737-082-39
; Sequence 39, Application US/10737082
; Publication No. US20050130170A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2032
; CURRENT APPLICATION NUMBER: US/10/737,082
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 52746
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-082-39

Query Match      68.6%; Score 19.2; DB 22; Length 52746;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 CCCATCTCCTCANNATCCCTGCTGTGG 27
Db      49957 CCCACTCCACAGCATCCCTGCTGTGG 49983
```

```
RESULT 13
US-10-765-790-39
; Sequence 39, Application US/10765790
; Publication No. US20050130172A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2035
; CURRENT APPLICATION NUMBER: US/10/765,790
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 52746
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-39

Query Match      68.6%; Score 19.2; DB 22; Length 52746;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTG 27
    ||||| ||| ||||| |||||
Db 49957 CCCACCTCCACAGCATCCGAGCTGTG 49983

RESULT 14
US-10-437-963-62174/c
; Sequence 62174, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 62174
; LENGTH: 2739
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_63534C.1
US-10-437-963-62174

Query Match      67.1%; Score 18.8; DB 19; Length 2739;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATCTCCTCANNATCCCTGCTGTG 28
    ||||| ||||| ||||| |||||
Db 2585 ATATCTTCAGTATCCCTGCTGATGG 2561

RESULT 15
US-10-029-386-27304
```

```
; Sequence 27304, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27304
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 9.00e-73
; OTHER INFORMATION: EST_HUMAN HIT: RA160611.1, EVALUE 4.00e-76
; OTHER INFORMATION: NT HIT: AF251442.1, EVALUE 0.00e+00
US-10-029-386-27304

Query Match      66.4%; Score 18.6; DB 16; Length 482;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCANNATCCCTGCTGTG 28
    ||||| ||||| ||||| |||||
Db 50 CCCATCTCTTCATACTCACTGCTGTG 77

RESULT 16
US-09-864-761-27448/c
; Sequence 27448, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 27448
;; LENGTH: 486
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004816.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.92
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.88
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: NT HIT: U07747.1, EVALUE 1.00e-15
;; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 8.00e-73
;; OTHER INFORMATION: EST_HUMAN HIT: AAL60611.1, EVALUE 3.00e-76
US-09-864-761-27448

Query Match 66.4%; Score 18.6; DB 9; Length 486;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
|||||
DB 433 CCCATCTCTTCACTACTCAGTGTGG 406

RESULT 17
US-10-029-386-13604
;; Sequence 13604, Application US/10029386
;; Publication No. US20030194704A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Hanzel, David R.
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: ABOMICA-X-2
;; CURRENT APPLICATION NUMBER: US/10/029,386
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 34288
;; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 13604
;; LENGTH: 577
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO CHR14.3
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
;; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 1.00e-72
;; OTHER INFORMATION: NT HIT: g14749516, EVALUE 0.00e+00
;; OTHER INFORMATION: EST_HUMAN HIT: AAL60611.1, EVALUE 5.00e-76
US-10-029-386-13604

Query Match 66.4%; Score 18.6; DB 16; Length 577;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
|||||
DB 93 CCCATCTCTTCACTACTCAGTGTGG 120

RESULT 18
US-10-437-963-53513/c
;; Sequence 53513, Application US/10437963
;; Publication No. US20040123343A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa, Thomas J.
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Cao, Yongwei
;; APPLICANT: Wu, Wei
;; APPLICANT: Boukharov, Andrey A.
;; APPLICANT: Barbazuk, Brad
;; APPLICANT: Li, Ping
;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 53513
;; LENGTH: 2301
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_55706C.1
US-10-437-963-53513

Query Match 66.4%; Score 18.6; DB 19; Length 2301;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
|||||
DB 1933 CCCATCTCTTCATGATGATGATGATGG 1906

RESULT 19
US-10-322-281-484/c
;; Sequence 484, Application US/10322281
;; Publication No. US20040126762A1
;; GENERAL INFORMATION:
;; APPLICANT: David W. Morris
;; APPLICANT: Marc S. Malandro
;; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;; FILE REFERENCE: 529452001000
;; CURRENT APPLICATION NUMBER: US/10/322,281
;; CURRENT FILING DATE: 2002-12-17
;; NUMBER OF SEQ ID NOS: 866
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 484
;; LENGTH: 6412
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-10-322-281-484

Query Match 66.4%; Score 18.6; DB 19; Length 6412;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCCATCTCNCANNATCCCTGCTGTGG 28
|||||
DB 1558 CCCCACTCTCTCACTCTCCCTGCTGATGG 1531

RESULT 20
US-10-322-281-483/c
;; Sequence 483, Application US/10322281
;; Publication No. US20040126762A1
;; GENERAL INFORMATION:
;; APPLICANT: David W. Morris
;; APPLICANT: Marc S. Malandro


```
; Sequence 256653, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256653
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-256653

Query Match 65.0%; Score 18.2; DB 13; Length 1506;
Best Local Similarity 76.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 CATCTCTCANNATCCCTGCTGTGG 28
||||| ||| | |||||
Db 293 CATCTCTCACCAGTCTTGTGTGG 318

RESULT 25
US-10-027-632-256653
; Sequence 256653, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256653
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-256653
```

```
Query Match 65.0%; Score 18.2; DB 17; Length 1506;
Best Local Similarity 76.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 CATCTCTCANNATCCCTGCTGTGG 28
||||| ||| | |||||
Db 293 CATCTCTCACCAGTCTTGTGTGG 318

RESULT 26
US-10-357-930-30260
; Sequence 30260, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30260
; LENGTH: 1928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-30260

Query Match 65.0%; Score 18.2; DB 20; Length 1928;
Best Local Similarity 76.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCANNATCCCTGCTGTGTT 26
||||| ||| | |||||
Db 847 CCCCTCTCTCAGTCTTCTGTGTTT 872

RESULT 27
US-10-918-897-12/c
; Sequence 12, Application US/10918897
; Publication No. US20050009086A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferty, Robert
; TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and Treating P
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: DEX-0196
; CURRENT APPLICATION NUMBER: US/10/918,897
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US/09/807,201
; PRIOR FILING DATE: 2001-04-25
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; PRIOR APPLICATION NUMBER: PCT/US99/24331
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,737
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-918-897-12

Query Match 65.0%; Score 18.2; DB 21; Length 2385;
Best Local Similarity 76.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCTTCTGCTGTT 26
Db 1590 CCCCTCTCCTCAGTCTTCTGCTGTT 1565

RESULT 28
US-09-759-143-333/c
; Sequence 333, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCTTCTGCTGTT 26
Db 1455 CCCCTCTCCTCAGTCTTCTGCTGTT 1430

RESULT 30
US-09-822-827-333/c
; Sequence 333, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCCTCAGTCTTCTGCTGTT 26
Db 1455 CCCCTCTCCTCAGTCTTCTGCTGTT 1430

RESULT 31
US-09-232-880-333/c
; Sequence 333, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

```

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCCTCAGTCTTCTCTGCTGTT 26
Db 1455 CCCCTCTCTCCTCAGTCTTCTCTGCTGTT 1430

RESULT 32

US-09-895-793-333/c
; Sequence 333, Application US/09895793
; Publication No. US20020192763A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 333

; LENGTH: 3030

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-895-793-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCCTCAGTCTTCTCTGCTGTT 26
Db 1455 CCCCTCTCTCCTCAGTCTTCTCTGCTGTT 1430

RESULT 33

US-09-895-814-333/c
; Sequence 333, Application US/09895814
; Publication No. US20020193296A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C26

; CURRENT APPLICATION NUMBER: US/09/895,814

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 990

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 333

; LENGTH: 3030

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-895-814-333

Query Match 65.0%; Score 18.2; DB 9; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCCATCTCTCCTCAGTCTTCTCTGCTGTT 26
Db 1455 CCCCTCTCTCCTCAGTCTTCTCTGCTGTT 1430

RESULT 34

US-10-012-896-333/c

; Sequence 333, Application US/10012896
; Publication No. US20020183251A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-333

Query Match 65.0%; Score 18.2; DB 13; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTT 26
||| ||||| ||| ||||| |||||
Db 1455 CCCCTCTCCTCAGTCTTCTGCTGTT 1430

RESULT 35

US-10-010-940-333/c
; Sequence 333, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-010-940-333

Query Match 65.0%; Score 18.2; DB 14; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTT 26
||| ||||| ||| ||||| |||||
Db 1455 CCCCTCTCCTCAGTCTTCTGCTGTT 1430

RESULT 36

US-10-144-678A-333/c
; Sequence 333, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-144-678A-333

Query Match 65.0%; Score 18.2; DB 16; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTT 26
||| ||||| ||| ||||| |||||
Db 1455 CCCCTCTCCTCAGTCTTCTGCTGTT 1430

RESULT 37

US-10-294-025-333/c
; Sequence 333, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 3030
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-294-025-333

Query Match 65.0%; Score 18.2; DB 16; Length 3030;
Best Local Similarity 76.9%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CCCATCTCNTCANNATCCCTGCTGTT 26
||| ||||| ||| ||||| |||||
Db 1455 CCCCTCTCCTCAGTCTTCTGCTGTT 1430

RESULT 38

US-10-318-389-4/c
; Sequence 4, Application US/10318389
; Publication No. US20040121328A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF PHOSPHODIESTERASE 8A EXPRESSION
; FILE REFERENCE: PFS-0062
; CURRENT APPLICATION NUMBER: US/10/318,389
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 4
; LENGTH: 77777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2937..3926
; OTHER INFORMATION: n = A,T,C or G
US-10-318-389-4

Query Match 65.0%; Score 18.2; DB 19; Length 77777;
Best Local Similarity 76.9%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCATCTCNCANNATCCCTGCTGTT 26

Db 11216 CCCACCCCTCAACATCCCTGCTTTT 11191

RESULT 39

US-10-175-523-197
; Sequence 197, Application US/10175523
; Publication No. US2003009264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 81826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(81826)
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other
US-10-175-523-197

Query Match 65.0%; Score 18.2; DB 14; Length 81826;
Best Local Similarity 76.9%; Pred. No. 2.3e+02;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CCATCTCNCANNATCCCTGCTGTTG 27
Db 44815 CCATCACTTCACCAACGCTGCTGTTG 44840

RESULT 40

US-10-719-993-7053/c
; Sequence 7053, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7053
; LENGTH: 117985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-7053

Query Match 65.0%; Score 18.2; DB 20; Length 117985;
Best Local Similarity 76.9%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CCATCTCNCANNATCCCTGCTGTTG 27

Db 79562 CCATCTCATCTGTTTACCTGCTGTTG 79537

Search completed: July 31, 2005, 15:45:50
Job time : 351.5 secs

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 10:46:20 ; Search time 818 Seconds
(without alignments)
1658.614 Million cell updates/sec

Title: US-10-085-944-2
Perfect score: 28
Sequence: 1 aatatgctgaacggagagaaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	28	100.0	342	14	FLD2CPW2
2	28	100.0	840	14	AF360860
3	28	100.0	840	14	AF360861
4	28	100.0	840	14	AF360862
5	28	100.0	840	14	AF360863
6	28	100.0	2319	14	S66064
7	28	100.0	2325	14	AF469175
8	28	100.0	2325	14	AF469176
9	28	100.0	2325	14	AF509530
10	28	100.0	2325	14	AY044442
11	28	100.0	2357	6	AR232496
12	28	100.0	2357	14	DEN2NGC
13	28	100.0	2469	14	DENJAMA
14	28	100.0	2552	14	AY152036S1
15	28	100.0	2552	14	AY152040S1
16	28	100.0	2552	14	AY152044S1
17	28	100.0	2552	14	AY152048S1
18	28	100.0	2552	14	AY152052S1
19	28	100.0	2552	14	AY152056S1

20	28	100.0	2552	14	AY152060S1	AY152060 Dengue vi
21	28	100.0	2552	14	AY152064S1	AY152064 Dengue vi
22	28	100.0	2552	14	AY152068S1	AY152068 Dengue vi
23	28	100.0	2552	14	AY152072S1	AY152072 Dengue vi
24	28	100.0	2552	14	AY152076S1	AY152076 Dengue vi
25	28	100.0	2552	14	AY152080S1	AY152080 Dengue vi
26	28	100.0	2552	14	AY152084S1	AY152084 Dengue vi
27	28	100.0	2552	14	AY152088S1	AY152088 Dengue vi
28	28	100.0	2552	14	AY152092S1	AY152092 Dengue vi
29	28	100.0	2552	14	AY152096S1	AY152096 Dengue vi
30	28	100.0	2552	14	AY152100S1	AY152100 Dengue vi
31	28	100.0	2552	14	AY152104S1	AY152104 Dengue vi
32	28	100.0	2552	14	AY152108S1	AY152108 Dengue vi
33	28	100.0	2552	14	AY152112S1	AY152112 Dengue vi
34	28	100.0	2552	14	AY152116S1	AY152116 Dengue vi
35	28	100.0	2552	14	AY152120S1	AY152120 Dengue vi
36	28	100.0	2552	14	AY152124S1	AY152124 Dengue vi
37	28	100.0	2552	14	AY152128S1	AY152128 Dengue vi
38	28	100.0	2552	14	AY152132S1	AY152132 Dengue vi
39	28	100.0	2552	14	AY152136S1	AY152136 Dengue vi
40	28	100.0	2552	14	AY152140S1	AY152140 Dengue vi
41	28	100.0	2552	14	AY152144S1	AY152144 Dengue vi
42	28	100.0	2552	14	AY152148S1	AY152148 Dengue vi
43	28	100.0	2552	14	AY152152S1	AY152152 Dengue vi
44	28	100.0	2552	14	AY152156S1	AY152156 Dengue vi
45	28	100.0	2552	14	AY152160S1	AY152160 Dengue vi
46	28	100.0	2552	14	AY152164S1	AY152164 Dengue vi
47	28	100.0	2552	14	AY152168S1	AY152168 Dengue vi
48	28	100.0	2552	14	AY152172S1	AY152172 Dengue vi
49	28	100.0	2552	14	AY152176S1	AY152176 Dengue vi
50	28	100.0	2552	14	AY152180S1	AY152180 Dengue vi
51	28	100.0	2552	14	AY152184S1	AY152184 Dengue vi
52	28	100.0	2552	14	AY152188S1	AY152188 Dengue vi
53	28	100.0	2552	14	AY152192S1	AY152192 Dengue vi
54	28	100.0	2552	14	AY152196S1	AY152196 Dengue vi
55	28	100.0	2552	14	AY152200S1	AY152200 Dengue vi
56	28	100.0	2552	14	AY152204S1	AY152204 Dengue vi
57	28	100.0	2552	14	AY152208S1	AY152208 Dengue vi
58	28	100.0	2552	14	AY152212S1	AY152212 Dengue vi
59	28	100.0	2552	14	AY152216S1	AY152216 Dengue vi
60	28	100.0	2552	14	AY152220S1	AY152220 Dengue vi
61	28	100.0	2552	14	AY152224S1	AY152224 Dengue vi
62	28	100.0	2552	14	AY152228S1	AY152228 Dengue vi
63	28	100.0	2552	14	AY152232S1	AY152232 Dengue vi
64	28	100.0	2552	14	AY152236S1	AY152236 Dengue vi
65	28	100.0	2552	14	AY152240S1	AY152240 Dengue vi
66	28	100.0	2552	14	AY152244S1	AY152244 Dengue vi
67	28	100.0	2552	14	AY152248S1	AY152248 Dengue vi
68	28	100.0	2552	14	AY152252S1	AY152252 Dengue vi
69	28	100.0	2552	14	AY152256S1	AY152256 Dengue vi
70	28	100.0	2552	14	AY152260S1	AY152260 Dengue vi
71	28	100.0	2552	14	AY152264S1	AY152264 Dengue vi
72	28	100.0	2552	14	AY152268S1	AY152268 Dengue vi
73	28	100.0	2552	14	AY152272S1	AY152272 Dengue vi
74	28	100.0	2552	14	AY152276S1	AY152276 Dengue vi
75	28	100.0	2552	14	AY152280S1	AY152280 Dengue vi
76	28	100.0	2552	14	AY152284S1	AY152284 Dengue vi
77	28	100.0	2552	14	AY152288S1	AY152288 Dengue vi
78	28	100.0	2552	14	AY152292S1	AY152292 Dengue vi
79	28	100.0	2552	14	AY152296S1	AY152296 Dengue vi
80	28	100.0	2552	14	AY152300S1	AY152300 Dengue vi
81	28	100.0	2552	14	AY152304S1	AY152304 Dengue vi
82	28	100.0	2552	14	AY152308S1	AY152308 Dengue vi
83	28	100.0	2552	14	AY152312S1	AY152312 Dengue vi
84	28	100.0	2552	14	AY152316S1	AY152316 Dengue vi
85	28	100.0	2552	14	AY152320S1	AY152320 Dengue vi
86	28	100.0	2552	14	AY152324S1	AY152324 Dengue vi
87	28	100.0	2552	14	AY152328S1	AY152328 Dengue vi
88	28	100.0	2552	14	AY152332S1	AY152332 Dengue vi
89	28	100.0	2552	14	AY152336S1	AY152336 Dengue vi
90	28	100.0	2552	14	AY152340S1	AY152340 Dengue vi
91	28	100.0	2552	14	AY152344S1	AY152344 Dengue vi
92	28	100.0	2552	14	AY152348S1	AY152348 Dengue vi
93	28	100.0	2552	14	AY152352S1	AY152352 Dengue vi

93	28	100.0	2552	14	AY1523356S1	AY1523356 Dengue vi	166	28	100.0	10723	14	DEN2CGA	M29095 Dengue viru
94	28	100.0	2552	14	AY1523360S1	AY1523360 Dengue vi	167	28	100.0	10723	14	DEN2JAMCG	M20558 Dengue viru
95	28	100.0	3381	6	AR122077	AR122077 Sequence	168	28	100.0	10723	14	DENCMEMSA	M84728 Dengue viru
96	28	100.0	3381	6	AR122078	AR122078 Sequence	169	28	100.0	10723	14	DENCMEMSB	M84727 Dengue viru
97	28	100.0	3381	6	AR135737	AR135737 Sequence	170	28	100.0	10723	14	U87411	U87411 Dengue viru
98	28	100.0	3381	6	AR135738	AR135738 Sequence	171	28	100.0	10723	14	U87412	U87412 Dengue viru
99	28	100.0	3381	6	AR559088	AR559088 Sequence	172	28	100.0	10724	14	AF022434	AF022434 Dengue vi
100	28	100.0	3381	6	BD073455	BD073455 Recombina	173	28	100.0	10724	14	AF038402	AF038402 Dengue vi
101	28	100.0	3381	14	DVU31949	U31949 Dengue viru	174	28	100.0	10724	14	AF038403	AF038403 Dengue vi
102	28	100.0	3381	14	DVU31950	U31950 Dengue viru	175	28	100.0	10756	6	AX224225	AX224225 Sequence
103	28	100.0	3381	14	DVU31951	U31951 Dengue viru	176	28	100.0	15237	12	AY243469	AY243469 Chimeric
104	28	100.0	3381	14	DVU31952	U31952 Dengue viru	177	28	100.0	15239	12	AY243467	AY243467 Chimeric
105	28	100.0	3381	14	DVU89517	U89517 Dengue viru	178	28	100.0	15239	12	AY376438	AY376438 Dengue vi
106	28	100.0	3381	14	DVU89518	U89518 Dengue viru	179	28	100.0	15256	12	AY656168	AY656168 Chimeric
107	28	100.0	10597	14	DVI48721	AJ48721 Dengue vi	180	28	100.0	15268	12	AY243468	AY243468 Chimeric
108	28	100.0	10618	14	AF326826	AF326826 Dengue vi	181	28	100.0	15270	12	AY243466	AY243466 Chimeric
109	28	100.0	10618	14	AF326827	AF326827 Dengue vi	182	28	100.0	15270	12	AY648301	AY648301 Dengue vi
110	28	100.0	10648	6	AX224231	AX224231 Sequence	183	28	100.0	15287	12	AY656167	AY656167 Chimeric
111	28	100.0	10648	6	AX224233	AX224233 Sequence	184	26.4	94.3	1119	14	AY079174	AY079174 Dengue vi
112	28	100.0	10648	14	DENSTRA	M14931 Dengue viru	185	26.4	94.3	342	14	DEN2CPG	X65239 Dengue-2 vi
113	28	100.0	10649	14	AF326573	AF326573 Dengue vi	186	26.4	94.3	342	14	DV1CAPSID	X70952 Dengue viru
114	28	100.0	10649	14	AF326825	AF326825 Dengue vi	187	26.4	94.3	342	14	FLD2CPM1	X51708 Dengue-2 vi
115	28	100.0	10649	14	AF375822	AF375822 Dengue vi	188	26.4	94.3	342	14	FLD2CPM3	X51710 Dengue-2 vi
116	28	100.0	10665	14	AF289029	AF289029 Dengue vi	189	26.4	94.3	479	14	AY079173	AY079173 Dengue vi
117	28	100.0	10674	14	AF100465	AF100465 Dengue vi	190	26.4	94.3	502	14	AF538029	AF538029 Dengue vi
118	28	100.0	10674	14	AF100467	AF100467 Dengue vi	191	26.4	94.3	506	14	DEN1CPMP	AF538029 Dengue vi
119	28	100.0	10674	14	AF100468	AF100468 Dengue vi	192	26.4	94.3	960	14	S75335	S75335 Dengue viru
120	28	100.0	10674	14	AF100469	AF100469 Dengue vi	193	26.4	94.3	2325	14	S64849	S64849 C...E Ideng
121	28	100.0	10682	14	AF100466	AF100466 Dengue vi	194	26.4	94.3	2419	14	DENPPSP	D00561 Dengue viru
122	28	100.0	10684	14	AF100462	AF100462 Dengue vi	195	26.4	94.3	2461	14	DENP83	D00501 Dengue viru
123	28	100.0	10685	14	AF100459	AF100459 Dengue vi	196	26.4	94.3	2474	14	DENCCV	D00502 Dengue viru
124	28	100.0	10685	14	AF100460	AF100460 Dengue vi	197	26.4	94.3	2474	14	DENTAH	AY152312 Dengue vi
125	28	100.0	10685	14	AF100461	AF100461 Dengue vi	198	26.4	94.3	2552	14	AY152312S1	AY152312 Dengue vi
126	28	100.0	10685	14	AF100463	AF100463 Dengue vi	199	26.4	94.3	2887	14	AY277652	AY277652 Dengue vi
127	28	100.0	10685	14	AF100464	AF100464 Dengue vi	200	26.4	94.3	2887	14	AY277653	AY277653 Dengue vi
128	28	100.0	10703	14	DENRCG	M19197 Dengue viru	201	26.4	94.3	2887	14	AY277654	AY277654 Dengue vi
129	28	100.0	10717	6	AX224217	AX224217 Sequence	202	26.4	94.3	2887	14	AY277656	AY277656 Dengue vi
130	28	100.0	10722	14	AF208496	AF208496 Dengue vi	203	26.4	94.3	2887	14	AY277657	AY277657 Dengue vi
131	28	100.0	10722	14	AF489932	AF489932 Dengue vi	204	26.4	94.3	2887	14	AY277658	AY277658 Dengue vi
132	28	100.0	10723	6	AX224219	AX224219 Sequence	205	26.4	94.3	2887	14	AY277659	AY277659 Dengue vi
133	28	100.0	10723	6	AX224221	AX224221 Sequence	206	26.4	94.3	2887	14	AY277660	AY277660 Dengue vi
134	28	100.0	10723	6	AX224223	AX224223 Sequence	207	26.4	94.3	2887	14	AY277661	AY277661 Dengue vi
135	28	100.0	10723	6	AX224235	AX224235 Sequence	208	26.4	94.3	2887	14	AY277662	AY277662 Dengue vi
136	28	100.0	10723	14	AB122020	AB122020 Dengue vi	209	26.4	94.3	2887	14	AY277663	AY277663 Dengue vi
137	28	100.0	10723	14	AB122021	AB122021 Dengue vi	210	26.4	94.3	3745	14	DEN1EMCNS	M23027 Dengue viru
138	28	100.0	10723	14	AB122022	AB122022 Dengue vi	211	26.4	94.3	10014	14	AY373427	AY373427 Dengue vi
139	28	100.0	10723	14	AB189122	AB189122 Dengue vi	212	26.4	94.3	10014	14	AY376738	AY376738 Dengue vi
140	28	100.0	10723	14	AB189123	AB189123 Dengue vi	213	26.4	94.3	10705	14	AY145123	AY145123 Dengue vi
141	28	100.0	10723	14	AB189124	AB189124 Dengue vi	214	26.4	94.3	10717	14	DENT18EQ	M87512 Dengue viru
142	28	100.0	10723	14	AF022435	AF022435 Dengue vi	215	26.4	94.3	10718	6	AY5711	AY5711 Sequence 1
143	28	100.0	10723	14	AF022436	AF022436 Dengue vi	216	26.4	94.3	10718	6	E06832	E06832 DNA sequenc
144	28	100.0	10723	14	AF022437	AF022437 Dengue vi	217	26.4	94.3	10721	14	AF298807	AF298807 Dengue vi
145	28	100.0	10723	14	AF022438	AF022438 Dengue vi	218	26.4	94.3	10721	14	AF298808	AF298808 Dengue vi
146	28	100.0	10723	14	AF022439	AF022439 Dengue vi	219	26.4	94.3	10721	14	AF309641	AF309641 Dengue vi
147	28	100.0	10723	14	AF022440	AF022440 Dengue vi	220	26.4	94.3	10723	6	AX224213	AX224213 Sequence
148	28	100.0	10723	14	AF022441	AF022441 Dengue vi	221	26.4	94.3	10723	6	AX224215	AX224215 Sequence
149	28	100.0	10723	14	AF119661	AF119661 Dengue vi	222	26.4	94.3	10733	14	AY145122	AY145122 Dengue vi
150	28	100.0	10723	14	AF169678	AF169678 Dengue vi	223	26.4	94.3	10735	6	AX224209	AX224209 Sequence
151	28	100.0	10723	14	AF169679	AF169679 Dengue vi	224	26.4	94.3	10735	6	AX224211	AX224211 Sequence
152	28	100.0	10723	14	AF169680	AF169680 Dengue vi	225	26.4	94.3	10735	14	AB074761	AB074761 Dengue vi
153	28	100.0	10723	14	AF169681	AF169681 Dengue vi	226	26.4	94.3	10735	14	AB074761	AB074761 Dengue vi
154	28	100.0	10723	14	AF169682	AF169682 Dengue vi	227	26.4	94.3	10735	14	AB178040	AB178040 Dengue vi
155	28	100.0	10723	14	AF169683	AF169683 Dengue vi	228	26.4	94.3	10735	14	AB189120	AB189120 Dengue vi
156	28	100.0	10723	14	AF169684	AF169684 Dengue vi	229	26.4	94.3	10735	14	AB189121	AB189121 Dengue vi
157	28	100.0	10723	14	AF169685	AF169685 Dengue vi	230	26.4	94.3	10735	14	AB189121	AB189121 Dengue vi
158	28	100.0	10723	14	AF169686	AF169686 Dengue vi	231	26.4	94.3	10735	14	AF180817	AF180817 Dengue vi
159	28	100.0	10723	14	AF169687	AF169687 Dengue vi	232	26.4	94.3	10735	14	AF180818	AF180818 Dengue vi
160	28	100.0	10723	14	AF169688	AF169688 Dengue vi	233	26.4	94.3	10735	14	AF226685	AF226685 Dengue vi
161	28	100.0	10723	14	AF204177	AF204177 Dengue vi	234	26.4	94.3	10735	14	AF226686	AF226686 Dengue vi
162	28	100.0	10723	14	AF204178	AF204178 Dengue vi	235	26.4	94.3	10735	14	AF226687	AF226687 Dengue vi
163	28	100.0	10723	14	AF276619	AF276619 Dengue vi	236	26.4	94.3	10735	14	AF311956	AF311956 Dengue vi
164	28	100.0	10723	14	AF359579	AF359579 Dengue vi	237	26.4	94.3	10735	14	AF311957	AF311957 Dengue vi
165	28	100.0	10723	14	AY037116	AY037116 Dengue vi	238	26.4	94.3	10735	14	AF350498	AF350498 Dengue vi

239	26.4	94.3	10735	14	AF513110	AF514876	Dengue vi	312	23.2	82.9	318	14	AF495895	Dengue vi
240	26.4	94.3	10735	14	AF514876	AF514878	Dengue vi	313	23.2	82.9	318	14	AF495902	Dengue vi
241	26.4	94.3	10735	14	AF514878	AF514883	Dengue vi	314	23.2	82.9	1050	14	AB010982	Dengue vi
242	26.4	94.3	10735	14	AF514883	AF514885	Dengue vi	315	23.2	82.9	1050	14	AB010983	Dengue vi
243	26.4	94.3	10735	14	AF514885	AF514889	Dengue vi	316	23.2	82.9	1050	14	AB010984	Dengue vi
244	26.4	94.3	10735	14	AF514889	AF5145121	Dengue vi	317	23.2	82.9	1050	14	AB010985	Dengue vi
245	26.4	94.3	10735	14	AF5145121	AF5145121	Dengue vi	318	23.2	82.9	1050	14	AB010986	Dengue vi
246	26.4	94.3	10735	14	AF5206457	AY206457	Dengue vi	319	23.2	82.9	1050	14	AB010987	Dengue vi
247	26.4	94.3	10735	14	AY206457	AY206457	Dengue vi	320	23.2	82.9	1050	14	AB010988	Dengue vi
248	26.4	94.3	10735	14	AY206457	AY206457	Dengue vi	321	23.2	82.9	1050	14	AB010989	Dengue vi
249	26.4	94.3	10735	14	DVU88535	U88535	Dengue vi	322	23.2	82.9	1050	14	AB010990	Dengue vi
250	26.4	94.3	10735	14	DVU88536	U88536	Dengue vi	323	22.2	79.3	240609	14	CR387997	Danio rer
251	26.4	94.3	10735	14	DVU88537	U88537	Dengue vi	324	22	78.6	72	6	AX573313	Sequence
252	26	92.9	26	6	AX042245	AX042245	Sequence	325	21.6	77.1	3381	14	DVU88237	U88237
253	24.8	88.6	290	14	AY079175	AY079175	Dengue vi	326	20.4	72.9	497	14	AF538027	Dengue vi
254	24.8	88.6	318	14	AF495890	AF495890	Dengue vi	327	20.4	72.9	62381	5	BX640594	Zebrafish
255	24.8	88.6	318	14	AF495892	AF495892	Dengue vi	328	20.4	72.9	191426	2	BX927352	Danio rer
256	24.8	88.6	318	14	AF495893	AF495893	Dengue vi	329	20	71.4	11064	14	AY453412	AY453412
257	24.8	88.6	318	14	AF495894	AF495894	Dengue vi	330	20	71.4	11066	14	AY453411	AY453411
258	24.8	88.6	318	14	AF495896	AF495896	Dengue vi	331	20	71.4	302050	1	AP006568	Gloeobact
259	24.8	88.6	318	14	AF495897	AF495897	Dengue vi	332	19.6	70.0	110000	8	CR380953	Continuation (8 of
260	24.8	88.6	318	14	AF495898	AF495898	Dengue vi	333	19.6	70.0	154341	5	CR381651	Continuation (8 of
261	24.8	88.6	318	14	AF495899	AF495899	Dengue vi	334	19.6	70.0	187785	2	CR788293	CR381651 Zebrafish
262	24.8	88.6	318	14	AF495901	AF495901	Dengue vi	335	19.6	70.0	209785	2	AC109497	CR788293 Danio rer
263	24.8	88.6	318	14	AF495903	AF495903	Dengue vi	336	19.2	68.6	1081	8	AY085057	AC109497 Mus muscu
264	24.8	88.6	318	14	AF495904	AF495904	Dengue vi	337	19.2	68.6	1920	8	YSP2FS	AY085057 Arabidops
265	24.8	88.6	318	14	AF495905	AF495905	Dengue vi	338	19.2	68.6	18991	8	SPC2FS	AY085057 Arabidops
266	24.8	88.6	318	14	AF495906	AF495906	Dengue vi	339	19.2	68.6	66303	9	BX470173	AY085057 Arabidops
267	24.8	88.6	495	14	AF008555	AF008555	Dengue vi	340	19.2	68.6	80167	8	AB022216	AL157874 S.pombe c
268	24.8	88.6	1050	14	AB038465	AB038465	Dengue vi	341	19.2	68.6	144648	9	AL391832	BX470173 Human DNA
269	24.8	88.6	1050	14	AB038466	AB038466	Dengue vi	342	19.2	68.6	172138	2	AC064796	AB022216 Arabidops
270	24.8	88.6	1050	14	AB038467	AB038467	Dengue vi	343	19.2	68.6	209384	2	AC064796	AB022216 Arabidops
271	24.8	88.6	1050	14	AB038468	AB038468	Dengue vi	344	19.2	68.6	237669	2	AC146821	AL391832 Human DNA
272	24.8	88.6	1050	14	AB038469	AB038469	Dengue vi	345	19	67.9	19	6	CQ789608	AC064796 Homo sapi
273	24.8	88.6	1050	14	AB038470	AB038470	Dengue vi	346	19	67.9	110000	2	AP006493	AC146821 Otolomur
274	24.8	88.6	1050	14	AB038471	AB038471	Dengue vi	347	19	67.9	130130	2	AC117804	CQ789608 Sequence
275	24.8	88.6	1050	14	AB038472	AB038472	Dengue vi	348	19	67.9	144319	2	AC117804	Continuation (2 of
276	24.8	88.6	1050	14	AB038473	AB038473	Dengue vi	349	19	67.9	165158	2	AC117804	AC117804 Mus muscu
277	24.8	88.6	1050	14	AB038474	AB038474	Dengue vi	350	19	67.9	165158	2	AC117804	AC117804 Mus muscu
278	24.8	88.6	1050	14	AB038475	AB038475	Dengue vi	351	19	67.9	166490	9	AL359438	AC117804 Mus muscu
279	24.8	88.6	1050	14	AB038476	AB038476	Dengue vi	352	19	67.9	169243	2	BX510323	AC117804 Mus muscu
280	24.8	88.6	1050	14	AB038477	AB038477	Dengue vi	353	19	67.9	209319	2	AC107799	AL359438 Human DNA
281	24.8	88.6	1050	14	AB038478	AB038478	Dengue vi	354	19	67.9	21505	10	AL844166	BX510323 Danio rer
282	24.8	88.6	1050	14	AB038479	AB038479	Dengue vi	355	19	67.9	21505	6	CQ789608	AL928631 Mouse DNA
283	24.8	88.6	2297	14	DENENVAA	M86733	Dengue vi	356	19	67.9	227781	2	AC132915	AC107799 Mus muscu
284	24.8	88.6	2880	14	AY099338S1	AY099338	Dengue vi	357	19	67.9	243627	2	AC132915	AL928631 Mouse DNA
285	24.8	88.6	2880	14	AY099339S1	AY099339	Dengue vi	358	19	67.9	270916	2	AC135523	AC132915 Mus muscu
286	24.8	88.6	2880	14	AY099340S1	AY099340	Dengue vi	359	18.8	67.1	56051	2	AC101777	AC135523 Rattus no
287	24.8	88.6	2880	14	AY099341S1	AY099341	Dengue vi	360	18.8	67.1	93398	8	AP006356	AC101777 Homo sapi
288	24.8	88.6	2880	14	AY099342S1	AY099342	Dengue vi	361	18.6	66.4	1145	6	AR504859	AP006356 Lotus cor
289	24.8	88.6	2887	14	AY277655	AY277655	Dengue vi	362	18.6	66.4	1153	5	AY190725	AR504859 Sequence
290	24.8	88.6	3000	14	DENPSAA	M25277	Dengue vi	363	18.6	66.4	2950	3	BT011150	AY190725 Pagrus ma
291	24.8	88.6	10696	14	AF317645	AF317645	Dengue vi	364	18.6	66.4	3002	6	CQ614256	BT011150 Drosophil
292	24.8	88.6	10696	14	DENCMC	M93130	Dengue type	365	18.6	66.4	7264	6	CQ614256	CQ614256 Sequence
293	24.8	88.6	10699	6	AX224227	AX224227	Sequence	366	18.6	66.4	8247	1	AB070943	CQ614256 Sequence
294	24.8	88.6	10699	6	AX224229	AX224229	Sequence	367	18.6	66.4	16832	1	AB070943	AB070943 Streptomy
295	24.8	88.6	10703	14	AB1679147	AB1679147	Dengue vi	368	18.6	66.4	18788	1	AY271621	AB070943 Streptomy
296	24.8	88.6	10707	14	AB189125	AB189125	Dengue vi	369	18.6	66.4	34733	3	CED2089	AY271621 Pseudomona
297	24.8	88.6	10707	14	AB189126	AB189126	Dengue vi	370	18.6	66.4	48744	2	AC014368	236948 Caenorhabdi
298	24.8	88.6	10707	14	AB189127	AB189127	Dengue vi	371	18.6	66.4	64168	4	AY152834	AC014368 Drosophil
299	24.8	88.6	10707	14	AB189128	AB189128	Dengue vi	372	18.6	66.4	85338	3	AC004279	AY152834 Felis cat
300	24.8	88.6	10707	14	AY099336	AY099336	Dengue vi	373	18.6	66.4	93121	2	DMR48A1	AC004279 Drosophil
301	24.8	88.6	10707	14	AY099337	AY099337	Dengue vi	374	18.6	66.4	100248	2	AC013150	AL121844 Drosophil
302	24.8	88.6	10707	14	AY648961	AY648961	Dengue vi	375	18.6	66.4	110000	2	AC128221	AC013150 Drosophil
303	24.8	88.6	10707	14	AY662691	AY662691	Dengue vi	376	18.6	66.4	112895	9	AC107210	Continuation (2 of
304	24.8	88.6	10735	14	AY277664	AY277664	Dengue vi	377	18.6	66.4	124456	2	AC017830	AC107210 Homo sapi
305	24.8	88.6	15145	12	AY656170	AY656170	Dengue vi	378	18.6	66.4	145952	3	CR003675	AC017830 Drosophil
306	24.8	88.6	15176	12	AY656169	AY656169	Dengue vi	379	18.6	66.4	159862	2	CR788253	AC003675 Drosophil
307	23.8	85.0	318	14	AF495900	AF495900	Dengue vi	380	18.6	66.4	161579	3	AC010212	CR788253 Danio rer
308	23.4	83.6	501	14	AF538025	AF538025	Dengue vi	381	18.6	66.4	162299	2	AC079086	AC010212 Drosophil
309	23.4	83.6	501	14	AF538026	AF538026	Dengue vi	382	18.6	66.4	167912	3	AC007650	AC079086 Homo sapi
310	23.2	82.9	318	14	AF495889	AF495889	Dengue vi	383	18.6	66.4	173380	3	AC099011	AC007650 Drosophil
311	23.2	82.9	318	14	AF495891	AF495891	Dengue vi	384	18.6	66.4	177199	5	BX547933	AC099011 Zebrafish

Department of Genetics and Cellular Biology, 5910 Kuala Lumpur, Malaysia
 See <M15075> and <M19197> for previously reported sequence. See <X51708> and <X51710> for capsid protein sequences of M1 and M3.
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 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 2
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 LOCUS
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 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Dengue virus type 2
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Dengue virus group.
 1 (bases 1 to 840)
 Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
 Holmes,E.C. and Gould,E.A.
 Molecular epidemiology of dengue type 2 virus in Venezuela:
 evidence for in situ virus evolution and recombination
 J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
 21571640
 11714970
 PUBLISHED
 REFERENCE
 2 (bases 1 to 840)
 Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
 Holmes,E.C. and Gould,E.A.
 Direct Submission
 Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
 Oxford OX2 6UD, England
 Location/Qualifiers
 1..840
 /organism="Dengue virus type 2"
 /mol_type="genomic RNA"
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RESULT 4
 AF360862

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RESULT 3
 AF360861
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Dengue virus type 2
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Flavivirus; Dengue virus group.
 1 (bases 1 to 840)
 Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
 Holmes,E.C. and Gould,E.A.
 Molecular epidemiology of dengue type 2 virus in Venezuela:
 evidence for in situ virus evolution and recombination
 J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
 21571640
 11714970
 PUBLISHED
 REFERENCE
 2 (bases 1 to 840)
 Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
 Holmes,E.C. and Gould,E.A.
 Direct Submission
 Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
 Oxford OX2 6UD, England
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 QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 40 AATATGCTGAACCGCGAGAGAAACCGCG 67

RESULT 4
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LOCUS AF360862 840 bp ss-RNA linear VRL 11-FEB-2002
DEFINITION Dengue virus type 2 isolate LARD1910 polyprotein gene, partial cds.
ACCESSION AF360862
VERSION AF360862.1 GI:18644125
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 840)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
JOURNAL 21571640
MEDLINE
PUBMED 11714970
REFERENCE
2 (bases 1 to 840)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
AUTHORS Direct Submission
TITLE Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
JOURNAL Oxford OX2 6UD, England
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1. .840
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAACCGCG 67

RESULT 5
AF360863
LOCUS AF360863 840 bp ss-RNA linear VRL 11-FEB-2002
DEFINITION Dengue virus type 2 isolate LARD1996 polyprotein gene, partial cds.
ACCESSION AF360863
VERSION AF360863.1 GI:18644127
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 840)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
JOURNAL 21571640
MEDLINE
PUBMED 11714970

REFERENCE
AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 6UD, England
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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 40 AATATGCTGAACCGGAGAGAACCGCG 67

RESULT 6
S66064
LOCUS S66064 2319 bp DNA linear VRL 04-DEC-1993
DEFINITION structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic,
2319 nt].
ACCESSION S66064
VERSION S66064.1 GI:432575
KEYWORDS
SOURCE
ORGANISM
Dengue virus type 4
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2319)
Kawano,H., Rostapehrov,V., Rosen,L. and Lai,C.J.
TITLE Genetic determinants of dengue type 4 virus neurovirulence for mice
J. Virol. 67 (11), 6567-6575 (1993)
JOURNAL 94016840
MEDLINE
PUBMED 8411360
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138430] from the original journal article.
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TVTYECPLLVNTEPIDWCNLTSAWNYGTCTQSGERRERKRSVALTPHSGMGLT

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SYGRCVCGNRRDFVGVSGCAWVDSVLEHGGCVTTMAQCKPFLDELKTRAKVAL
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2319;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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RESULT 7

AF469175 2325 bp RNA linear VRL 20-FEB-2002
LOCUS Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
DEFINITION
ACCESSION AF469175
VERSION AF469175.1 GI:18766554
KEYWORDS
SOURCE
ORGANISM

Dengue virus type 2
Dengue virus type 2
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
Unpublished
2 (bases 1 to 2325)
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.

REFERENCE

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
Location/Qualifiers
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FEATURES

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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2325;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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RESULT 8

AF469176 2325 bp RNA linear VRL 20-FEB-2002
LOCUS Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
DEFINITION
ACCESSION AF469176
VERSION AF469176.1 GI:18766556
KEYWORDS
SOURCE
ORGANISM

Dengue virus type 2
Dengue virus type 2
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.
Structural genes of dengue virus type 2 strain GD24/93 isolate from
Nanhai, Guangdong, China
Unpublished
2 (bases 1 to 2325)
Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
Zhao, W.Z.

REFERENCE

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
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100.0%; Score 28; DB 14; Length 2325;
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2325;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
|||||

RESULT 9
AF509530
LOCUS AF509530 2325 bp RNA linear VRL 22-MAY-2002
DEFINITION Dengue virus type 2 polyprotein gene, partial cds.
ACCESSION AF509530
VERSION AF509530.1 GI:21070436
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2325)
AUTHORS Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
TITLE Isolation, identification and sequence analyses of dengue virus type 2 strain GD19/2001
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2325)
AUTHORS Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Microbiology Department, The Military Medical Institute of Guangzhou Military District, Dongguanhuang Road, Guangzhou 510507, China
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 40 AATATGCTGAACCGCAGAGAAACCGCG 67
|||||

RESULT 10
AY044442
LOCUS AY044442 2325 bp ss-RNA linear VRL 10-FEB-2002
DEFINITION Dengue virus type 2 strain Maraz polyprotein gene, partial cds.
ACCESSION AY044442
VERSION AY044442.1 GI:18643733
SOURCE
ORGANISM
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2325)

AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
TITLE Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
11714970
REFERENCE 2 (bases 1 to 2325)
AUTHORS Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.M.,
Holmes,E.C. and Gould,E.A.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield Road, Oxford OX1 3SR, United Kingdom
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCAGAGAAACCGCG 28
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Db 40 AATATGCTGAACCGCAGAGAAACCGCG 67
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RESULT 11
AR232496
LOCUS AR232496 2357 bp RNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6455509.
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2357)
AUTHORS Kochel,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
TITLE Dengue nucleic acid vaccines that induce neutralizing antibodies

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JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
Source 1. .2357
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Db 60 AATATGCTGAACGCGAGAGAAACCGCG 87

RESULT 12
DEN2NGC 2357 bp RNA linear VRL 29-MAY-2002
LOCUS Dengue virus type 2 gene for polyprotein, partial cds, strain:New
DEFINITION Guinea C.
ACCESSION D00346
VERSION D00346.1 GI:221230
KEYWORDS Dengue virus type 2
SOURCE Dengue virus type 2
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2357)
AUTHORS Gruenberg, A., Woo, W.S., Biedrzycka, A. and Wright, P.J.
TITLE Partial nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue virus type 2, New Guinea C and
PUO-218 strains
JOURNAL J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
MEDLINE 88259474
PUBMED 3385407
COMMENT Nucleotide 1 in the NCG sequence corresponds to nucleotide 77
counting from the 5' end of the DEN-2(JAM) sequence.
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JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 60 AATATGCTGAACGCGAGAGAAACCGCG 87

RESULT 13
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DEFINITION M15075
ACCESSION M15075.1 GI:323650
KEYWORDS Dengue virus type 2
SOURCE Dengue virus type 2
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2469)
AUTHORS Deubel, V., Kinney, R.M. and Trent, D.W.
TITLE Nucleotide sequence and deduced amino acid sequence of the
structural proteins of dengue type 2 virus, Jamaica genotype
Virology 155 (2), 365-377 (1986)
JOURNAL 87071658
MEDLINE 3024394
PUBMED
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JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db      136 AATATGCTGAAACCGGAGAGAAACCGG 163
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Dengue virus type 4 D4_20_1998 polyprotein precursor, gene, partial cds.
AY152036S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION
ACCESSION AY152036
VERSION AY152036.1 GI:28170806
KEYWORDS
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JOURNAL
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RESULT 15
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LOCUS

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ORGANISM Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 17
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LOCUS
DEFINITION Dengue virus type 4 D4.14_1998 polyprotein precursor, gene, partial
cdd.
AV152048
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus

ORGANISM Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 17
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LOCUS
DEFINITION Dengue virus type 4 D4.14_1998 polyprotein precursor, gene, partial
cdd.
AV152048
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 18
AV152052S1
LOCUS
DEFINITION Dengue virus type 4 D4.12_1998 polyprotein precursor, gene, partial
cdd.
AV152052
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBLISHED 12832629
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio

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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 22
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ACCESSION AY152064
VERSION AY152064.1
KEYWORDS GI:28170867
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.14;
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

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ACCESSION AY152068
VERSION AY152068.1
KEYWORDS GI:28170878
SEGMENT 1 of 4
SOURCE Dengue virus type 4 (DEN-4)
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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LOCUS

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ACCESSION AY152072

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

i of 4

Dengue virus type 4 (DEN-4)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

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ORIGIN

Query Match

Best Local Similarity

100.0%; Score 28; DB 14; Length 2552;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches

28; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy

1 AATATGCTGAACCGGAGAGAAACCGCG 28

|||||

Db

37 AATATGCTGAACCGGAGAGAAACCGCG 64

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RESULT 24

AY152076S1

LOCUS

DEFINITION

Dengue virus type 4 D4.48_1998 polyprotein precursor, gene, partial

cds.

ACCESSION AY152076

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

i of 4

Dengue virus type 4 (DEN-4)

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,

Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

FEATURES

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ORIGIN

Query Match

Best Local Similarity

100.0%; Score 28; DB 14; Length 2552;

Matches 28; Conservative

0; Mismatches

0; Indels

0; Gaps

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Qy

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Db

37 AATATGCTGAACCGGAGAGAAACCGCG 64

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LOCUS
DEFINITION
  Dengue virus type 4 D4.15_1998 polyprotein precursor, gene, partial cds.
ACCESSION
  AY152080
VERSION
  AY152080.1 GI:28170905
KEYWORDS
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SOURCE
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ORGANISM
  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Flavivirus; Dengue virus group.
REFERENCE
  1 (bases 1 to 2552)
  Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
  Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
  Selection-Driven Evolution of Emergent Dengue Virus
  Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
  12832629
PUBMED
  12832629
TITLE
  Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
  Piedras, PO Box 23360, San Juan 00931, Puerto Rico
JOURNAL
  Location/Qualifiers
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DEFINITION
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ACCESSION
  AY152084
VERSION
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KEYWORDS
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SOURCE
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ORGANISM
  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE
  1 (bases 1 to 2552)
  Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
  Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
  Selection-Driven Evolution of Emergent Dengue Virus
  Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
  12832629
PUBMED
  12832629
TITLE
  Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
  Piedras, PO Box 23360, San Juan 00931, Puerto Rico
JOURNAL
  Location/Qualifiers
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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REFERENCE
  1 (bases 1 to 2552)
  Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
  Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
  Selection-Driven Evolution of Emergent Dengue Virus
  Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
  12832629
PUBMED
  12832629
TITLE
  Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
  Piedras, PO Box 23360, San Juan 00931, Puerto Rico
JOURNAL
  Location/Qualifiers
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Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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RESULT 29
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LOCUS
DEFINITION
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ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

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DEFINITION
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ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 31
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LOCUS
DEFINITION
Dengue virus type 4 D4.112.1995MQ polyprotein precursor, gene,
partial cds.

ACCESSION
AY152100.1
VERSION
AY152100.1
KEYWORDS
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SEGMENT
Dengue virus type 4 (DEN-4)
SOURCE
Dengue virus type 4
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

TITLE
JOURNAL
PUBMED
12832629
AUTHORS
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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DEFINITION
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partial cds.

ACCESSION
AY152100.1
VERSION
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KEYWORDS
1 of 4
SEGMENT
Dengue virus type 4 (DEN-4)
SOURCE
Dengue virus type 4
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

TITLE
JOURNAL
PUBMED
12832629
AUTHORS
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

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glycoprotein"

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Db 37 AATATGCTGAACCGCAGAGAAACCGCG 64
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ACCESSION AY152108
VERSION AY152108.1 GI:28170968
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1. of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGCAGAGAAACCGCG 64
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RESULT 33
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DEFINITION Dengue virus type 4 D4.36_1992 polyprotein precursor, gene, partial cds.
ACCESSION AY152112
VERSION AY152112.1 GI:28170977
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1. of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

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DEFINITION cds.
ACCESSION AY152116.1 GI:28170986
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Dengue virus type 4
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64

RESULT 35
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LOCUS Dengue virus type 4 D4.89_1994 polyprotein precursor, gene, partial
DEFINITION cds.
ACCESSION AY152120.1 GI:28170995
KEYWORDS 1 of 4
SEGMENT Dengue virus type 4 (DEN-4)
SOURCE Dengue virus type 4
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
REFERENCE 1 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Selection-Driven Evolution of Emergent Dengue Virus
JOURNAL Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
PUBMED 12832629
REFERENCE 2 (bases 1 to 2552)
AUTHORS Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Dengue virus type 4 D4.80_1994 polyprotein precursor, gene, partial
DEFINITION

12832629

2 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

Location/Qualifiers

1. .2552

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Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 39

AY152136S1

LOCUS

DEFINITION

AY152136S1 2552 bp RNA linear VRL 29-SEP-2003

Dengue virus type 4 D4.76.1994 polyprotein precursor, gene, partial cds.

ACCESSION

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

1 of 4

Dengue virus type 4 (DEN-4)

Dengue virus type 4

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

1 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Selection-Driven Evolution of Emergent Dengue Virus

Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629

2 (bases 1 to 2552)

Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

Direct Submission

Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

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ORGANISM	Dengue virus type 4 (DEN-4)	
REFERENCE		
AUTHORS	Viruses; SRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	
	1 (bases 1 to 2552)	
	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	
TITLE	Selection-Driven Evolution of Emergent Dengue Virus	
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)	
PUBMED	12832629	
REFERENCE		
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	
TITLE	Direct Submission	
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico	
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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.14;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	28	100.0	3381	2	AAX25114 Dengue vi
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27	26.4	94.3	10723	4	AAD14603
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C 62	18.4	65.7	11313	12	ADP86264
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C 64	18.4	65.7	11313	12	ADP86265
C 65	18.4	65.7	11313	12	ADP86268
C 66	18.4	65.7	11313	12	ADP86270
C 67	18.4	65.7	11313	12	ADP86271
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Adg93317	DEN1 (Pue
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Aad14604	Dengue vi
Aad14602	Attenuate
Aad14601	Wild-type
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Aac68744	Dengue vi
Aat75917	DEN-2 clo
Aad14610	Wild-type
Aad14611	Attenuate
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Aaf88836	Green flu
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Aaz36195	Nucleotid
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Ach40248	Human foe
Abx34665	Human cdn
Adq62907	Novel hum
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Acc72810	Human can
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c 97	18	64.3	14952	10	ACF69283	Acf69283 Photorhab	170	17.2	61.4	1960	5	ABV28010	Abv28010 Human pro
c 98	18	64.3	100779	10	ACF65386 ⁶	Continuation (7 of	171	17.2	61.4	1960	5	ABV22171	Abv22171 Human pro
c 99	18	64.3	110000	10	ACF67367 ²²	Continuation (23 o	172	17.2	61.4	2270	4	ABL27934	AbL27934 Drosophil
c 100	17.8	63.6	973	4	AAI16919	Aai16919 Human neu	173	17.2	61.4	2300	4	ABL27932	AbL27932 Drosophil
c 101	17.8	63.6	4822	4	ABL20414	AbL20414 Drosophil	174	17.2	61.4	3201	13	ADR15119	Adr15119 Rat elect
c 102	17.6	62.9	550	11	ACN90669	Acn90669 Breast ca	175	17.2	61.4	3319	2	AAT43076	Aat43076 Wheat ace
c 103	17.6	62.9	557	4	AAI12137	Aai12137 Human bre	176	17.2	61.4	3319	2	AAV34412	Aav34412 5' end fl
c 104	17.6	62.9	691	4	AAL21020	Aal21020 Human bre	177	17.2	61.4	24398	4	AAS01768	Aas01768 Drosophil
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c 106	17.6	62.9	695	3	AAZ53156	Aaz53156 Neisseria	179	17	60.7	435	11	ABD02565	Abd02565 Pseudomon
c 107	17.6	62.9	696	3	AAI15311	Aai15311 DNA encod	180	17	60.7	437	8	ABX37358	Abx37358 Bovine ES
c 108	17.6	62.9	838	11	ACN82318	Acn82318 Breast ca	181	17	60.7	473	6	ABN64425	Abn64425 Human can
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c 110	17.6	62.9	945	6	ABQ69758	Abq69758 Listeria	183	17	60.7	1202	3	AAC44984	Aac44984 Arabidops
c 111	17.6	62.9	966	6	ABQ67740	Abq67740 Listeria	184	17	60.7	1725	2	AAT60349	Aat60349 MAP kinas
c 112	17.6	62.9	966	6	ABQ67741	Abq67741 Listeria	185	17	60.7	1786	2	AAT60350	Aat60350 MAP kinas
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c 114	17.6	62.9	2485	12	ADO35406	Ado35406 Novel mou	187	17	60.7	1869	8	ADA68153	Ada68153 Arabidops
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c 120	17.6	62.9	110000	6	ABQ67196 ¹	Continuation (2 of	193	17	60.7	14000	4	AAS46232	Aas46232 DNA encod
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c 122	17.6	62.9	110000	6	ABQ69245 ²⁴	Continuation (27 o	195	16.8	60.0	69	12	ADN36694	Adn36694 West Nile
c 123	17.6	62.9	349980	3	AAF21607 ²⁶	Aaf21607 Neisseria	196	16.8	60.0	287	10	ABX82696	Abx82696 Corn ear-
c 124	17.4	62.1	356	5	AAF65359	Aaf65359 Novel hum	197	16.8	60.0	331	2	AAQ89698	Aaq89698 Transcrip
c 125	17.4	62.1	379	6	ABQ84757	Abq84757 Chlamydia	198	16.8	60.0	365	6	ABK51710	Abk51710 Partial c
c 126	17.4	62.1	379	6	ABQ78015	Abq78015 Chlamydia	199	16.8	60.0	366	8	ABQ76684	Abq76684 MNVcwt DN
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c 128	17.4	62.1	589	6	ABQ47607	Abq47607 Oligonucl	201	16.8	60.0	503	6	ABQ31108	Abq31108 Oligonucl
c 129	17.4	62.1	589	6	ABQ47606	Abq47606 Oligonucl	202	16.8	60.0	509	6	ABQ20645	Abq20645 Oligonucl
c 130	17.4	62.1	657	2	AAQ03640	Aaq03640 Cucumbe	203	16.8	60.0	509	6	ABQ20644	Abq20644 Oligonucl
c 131	17.4	62.1	691	6	ABQ52041	Abq52041 Oligonucl	204	16.8	60.0	621	5	AAS29124	Aas29124 cDNA enco
c 132	17.4	62.1	691	6	ABQ52040	Abq52040 Oligonucl	205	16.8	60.0	621	6	ABS68264	Abs68264 cDNA enco
c 133	17.4	62.1	774	8	ACA51992	Aca51992 Prokaryot	206	16.8	60.0	621	10	ADC25258	Adc25258 Human CDN
c 134	17.4	62.1	778	8	ACA48879	Aca48879 Prokaryot	207	16.8	60.0	672	5	AAS68401	Aas68401 DNA encod
c 135	17.4	62.1	1227	9	ADA30601	Ada30601 DNA encod	208	16.8	60.0	681	10	ABZ38190	Abz38190 N. gonorr
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c 137	17.4	62.1	2000	10	ACC61659	Acc61659 Gene sequ	210	16.8	60.0	716	6	ABQ40083	Abq40083 Oligonucl
c 138	17.4	62.1	2000	10	ADK64251	Adk64251 Disease t	211	16.8	60.0	716	6	ABQ40082	Abq40082 Oligonucl
c 139	17.4	62.1	2520	6	ABQ84758	Abq84758 Chlamydia	212	16.8	60.0	788	6	ABQ20794	Abq20794 Oligonucl
c 140	17.4	62.1	2520	6	ABQ78016	Abq78016 Chlamydia	213	16.8	60.0	788	6	ABQ20795	Abq20795 Oligonucl
c 141	17.4	62.1	2520	8	ABX99183	Abx99183 C. psittca	214	16.8	60.0	857	6	ABQ43221	Abq43221 Oligonucl
c 142	17.4	62.1	4017	4	ABL07760	AbL07760 Drosophil	215	16.8	60.0	857	6	ABQ43220	Abq43220 Oligonucl
c 143	17.4	62.1	5026	3	ABK64961	Abk64961 C. elegan	216	16.8	60.0	906	8	ACA41677	Aca41677 Prokaryot
c 144	17.4	62.1	5026	6	ABK84841	Abk84841 DNA fragm	217	16.8	60.0	936	11	ABD12893	Abd12893 Pseudomon
c 145	17.4	62.1	6612	3	AAC64963	Aac64963 C. elegan	218	16.8	60.0	1087	12	ADQ63330	Adq63330 Transcrip
c 146	17.4	62.1	6612	6	ABK84843	Abk84843 DNA fragm	219	16.8	60.0	1116	10	ADB55037	Adb55037 A. thalia
c 147	17.4	62.1	11207	3	AAC64960	Aac64960 C. elegan	220	16.8	60.0	1179	6	ABQ30075	Abq30075 Oligonucl
c 148	17.4	62.1	11207	6	ABK84840	Abk84840 Cognid K1	221	16.8	60.0	1179	6	ABQ30074	Abq30074 Oligonucl
c 149	17.4	62.1	11207	6	ABK84832	Abk84832 pDM2600 C	222	16.8	60.0	1257	8	ACA21389	Aca21389 Prokaryot
c 150	17.4	62.1	11438	6	ABK84831	Abk84831 pDM2600 C	223	16.8	60.0	1289	13	ADT41781	Adt41781 Bacterial
c 151	17.4	62.1	17678	4	ABL19341	AbL19341 Drosophil	224	16.8	60.0	1321	3	AAC39461	Aac39461 Arabidops
c 152	17.4	62.1	18011	4	ABL20689	AbL20689 Drosophil	225	16.8	60.0	1654	13	ADR65635	Adr65635 Cotton cd
c 153	17.4	62.1	27845	4	ABL20591	AbL20591 Drosophil	226	16.8	60.0	1657	6	ABQ70507	Abq70507 Listeria
c 154	17.4	62.1	31737	10	ACF67733	Acf67733 Photorhab	227	16.8	60.0	1746	11	ABD01202	Abd01202 Klebsiell
c 155	17.4	62.1	39726	9	AIL57448	Ail57448 Human NSD	228	16.8	60.0	2361	8	ACA41419	Aca41419 Prokaryot
c 156	17.4	62.1	48718	4	ABL20590	AbL20590 Drosophil	229	16.8	60.0	2615	10	ABZ39121	Abz39121 N. gonorr
c 157	17.4	62.1	63284	4	ABL20688	AbL20688 Drosophil	230	16.8	60.0	2615	4	AAAF4670	Aaf4670 Mouse MAR
c 158	17.4	62.1	71962	4	ABL19340	AbL19340 Drosophil	231	16.8	60.0	3210	12	ADI43146	Adi43146 Plant tra
c 159	17.4	62.1	110000	10	ACF65383 ²	Continuation (3 of	232	16.8	60.0	3210	12	ADO03245	Ado03245 Corn orth
c 160	17.4	62.1	115780	13	ABD332610 ⁰³	Continuation (4 of	233	16.8	60.0	3210	12	ADO62538	Ado62538 Transcrip
c 161	17.4	62.1	115780	13	ABD332610 ⁰³	Abd332610 Mouse can	234	16.8	60.0	3867	4	ABL28028	AbL28028 Drosophil
c 162	17.4	62.1	145068	13	ABD333090	Abd333090 Murine ca	235	16.8	60.0	5965	4	ABL05674	AbL05674 Human rep
c 163	17.4	62.1	235070	11	ACN45174	Acn45174 Human gen	236	16.8	60.0	5965	4	ABA07992	AbA07992 Human ova
c 164	17.2	61.4	300	4	ABL27933	AbL27933 Drosophil	237	16.8	60.0	10945	13	ADR32078	Adr32078 Genomic D
c 165	17.2	61.4	1050	8	ADA72690	Ada72690 Rice gene	238	16.8	60.0	10945	13	ADR62768	Adr62768 West Nile
c 166	17.2	61.4	1428	13	ADS57489	Ads57489 Bacterial	239	16.8	60.0	10945	13	ADR67768	Adr67768 West Nile

240	16.8	60.0	10962	12	ADK13681	Adk13681 West Nile	313	16.6	59.3	10091	2	AAV69642	Aav69642 Drosophil
241	16.8	60.0	10975	12	ADN98022	Adn98022 West Nile	314	16.6	59.3	25895	10	ADC86256	Adc86256 Human GPC
242	16.8	60.0	11029	8	ABZ68481	Abz68481 Nucleotid	315	16.6	59.3	31034	4	ABL13678	Ab13678 Drosophil
243	16.8	60.0	11029	10	ABV74821	Abv74821 West Nile	316	16.6	59.3	43011	12	ADN01941	Adn01941 Staphyloc
244	16.8	60.0	11029	12	ADN98023	Adn98023 West Nile	c 317	16.6	59.3	60873	3	AAA81469	Aaa81469 N. mening
245	16.8	60.0	12790	4	AAS46237	Aas46237 DNA encod	c 318	16.6	59.3	110000	3	AAA81490_12	Continuation (13 o
246	16.8	60.0	17651	4	AAS59519	Aas59519 Propionib	c 319	16.6	59.3	110000	10	ABS56450_02	Continuation (3 of
247	16.8	60.0	17651	4	ACF64448	Acf64448 Propionib	320	16.6	59.3	110000	3	ABS56454_06	Continuation (7 of
248	16.8	60.0	22345	4	ABL02352	Ab102352 Drosophil	c 321	16.6	59.3	110000	10	ABD32923_5	Continuation (6 of
c 249	16.8	60.0	38234	11	ACM45022	Adn45022 Human gen	c 322	16.6	59.3	134841	11	ACN45172_5	ACN45172 Mouse gen
c 250	16.8	60.0	46593	3	AAA81456	Aaa81456 N. mening	323	16.6	59.3	143899	6	AAA8138336	Ab138336 Genomic s
c 251	16.8	60.0	49767	3	AAA81458	Aaa81458 N. mening	c 324	16.6	59.3	152759	13	ABD33075	Abd33075 Human can
c 252	16.8	60.0	95914	13	ABD33444	Abd33444 Human can	c 325	16.6	59.3	348101	12	ADQ971146	Adq971146 Human can
c 253	16.8	60.0	110000	3	AAA81489_5	Continuation (6 of	326	16.6	59.3	349980	2	AAF21610	Aaf21610 Neisseria
c 254	16.8	60.0	110000	3	AAA81489_6	Continuation (7 of	327	16.6	58.6	214	6	ABR64434	AbR64434 Human ben
c 255	16.8	60.0	110000	3	AAA81489_7	Continuation (8 of	328	16.4	58.6	214	6	ABN95307	Abn95307 Gene #180
c 256	16.8	60.0	172325	3	AAF21613	Aaf21613 Neisseria	c 329	16.4	58.6	290	3	AAA00762	Aaa00762 Human col
c 257	16.8	60.0	188794	12	ADQ59476	Adq59476 Human can	c 330	16.4	58.6	316	13	ADS54663	AdS54663 Bacterial
c 258	16.8	60.0	349980	3	AAF21612	Aaf21612 Neisseria	c 331	16.4	58.6	364	2	AAQ559802	Aaq559802 Human bra
c 259	16.8	60.0	349980	3	AAF21612	Aaf21612 Neisseria	332	16.4	58.6	390	5	AAH65657	Aah65657 C glutami
c 260	16.6	59.3	100	8	ACD69720	Abd69720 E. coli K	333	16.4	58.6	390	8	ACA00090	ACA00090 C. glutam
c 261	16.6	59.3	297	10	ABX82062	Abx82062 Corn ear-	334	16.4	58.6	393	4	AAH76027	Aah76027 DNA encod
c 262	16.6	59.3	360	5	AAK54283	Aak54283 Murine tr	c 335	16.4	58.6	442	10	ADF80484	Adf80484 Leukaemia
c 263	16.6	59.3	409	4	AAK54136	Aak54136 Murine tr	c 336	16.4	58.6	475	4	AAI01740	Aai01740 Human rep
c 264	16.6	59.3	444	11	ADM65372	Adm65372 NRY polym	c 337	16.4	58.6	475	4	ABL97033	Ab197033 Human tes
c 265	16.6	59.3	487	10	ADC77133	Adc77133 DNA homol	c 338	16.4	58.6	504	6	ABQ30555	Abq30555 Oligonucle
c 266	16.6	59.3	487	10	ADK59424	Adk59424 Plant DNA	c 339	16.4	58.6	504	6	ABQ30554	Abq30554 Oligonucle
c 267	16.6	59.3	504	12	ACH74791	Ach74791 Human gen	c 340	16.4	58.6	612	5	AAH67960	Aah67960 C glutami
c 268	16.6	59.3	591	8	ABZ54114	Abz54114 Aspergill	c 341	16.4	58.6	614	6	ABQ50702	Abq50702 Oligonucle
c 269	16.6	59.3	669	8	ACF72930	Acf72930 Staphyloc	342	16.4	58.6	614	6	ABQ50703	Abq50703 Oligonucle
c 270	16.6	59.3	702	2	AAV74625	Aav74625 Staphyloc	c 343	16.4	58.6	615	8	ACA02097	ACA02097 C. glutam
c 271	16.6	59.3	768	10	ADC76882	Adc76882 DNA homol	c 344	16.4	58.6	621	13	ADS57054	AdS57054 Bacterial
c 272	16.6	59.3	792	10	ADH82410	Adh82410 Enterococ	c 345	16.4	58.6	630	4	ACA25520	Aca25520 Human ova
c 273	16.6	59.3	829	10	ABX06024	Abx06024 S. pneumo	c 346	16.4	58.6	631	8	ACA37473	Aca37473 Prokaryot
c 274	16.6	59.3	831	10	ABX06527	Abx06527 S. pneumo	c 347	16.4	58.6	657	6	ABQ31721	Abq31721 Oligonucle
c 275	16.6	59.3	851	2	AAV52494	Aav52494 Streptoco	c 348	16.4	58.6	657	6	ABQ31720	Abq31720 Oligonucle
c 276	16.6	59.3	876	2	AAQ04535	Aaq04535 Polypepti	c 349	16.4	58.6	682	6	ABQ65760	Abq65760 Arabidops
c 277	16.6	59.3	891	8	ACA47337	AcA47337 Prokaryot	c 350	16.4	58.6	742	11	ADL65988	AdL65988 C. glutam
c 278	16.6	59.3	909	8	ABZ51282	Abz51282 Aspergill	351	16.4	58.6	768	4	ASA24348	Aas24348 Human ova
c 279	16.6	59.3	932	3	ACA54942	Aca54942 Arabidops	352	16.4	58.6	778	5	AAH82937	Aah82937 Human ova
c 280	16.6	59.3	936	3	ACA35411	Aca35411 Arabidops	353	16.4	58.6	988	6	ABQ47291	Abq47291 Oligonucle
c 281	16.6	59.3	1058	10	ADC77137	Adc77137 DNA homol	c 354	16.4	58.6	988	6	ABQ47290	Abq47290 Oligonucle
c 282	16.6	59.3	1058	10	ADK59428	Adk59428 Plant DNA	c 355	16.4	58.6	1029	13	ADS55698	AdS55698 Bacterial
c 283	16.6	59.3	1058	10	ADK55693	Adk55693 Plant DNA	c 356	16.4	58.6	1037	3	AAQ52043	Aaq52043 Arabidops
c 284	16.6	59.3	1149	10	ABZ39764	Abz39764 N. gonorr	c 357	16.4	58.6	1137	13	AAQ50184	Aaq50184 Bacterial
c 285	16.6	59.3	1191	10	ADC77296	Adc77296 DNA homol	c 358	16.4	58.6	1359	5	AAH88887	Aah88887 DNA encod
c 286	16.6	59.3	1191	10	ADC77296	Adc77296 DNA homol	c 359	16.4	58.6	1361	12	ADJ74952	Adj74952 Marker ge
c 287	16.6	59.3	1200	8	ACA50147	AcA50147 Plant DNA	c 360	16.4	58.6	1361	12	ADN04871	Adn04871 Antipsori
c 288	16.6	59.3	1221	6	ABQ41561	Abq41561 Oligonucle	c 361	16.4	58.6	1361	13	ADP25040	AdP25040 PRO poly
c 289	16.6	59.3	1221	6	ABQ41560	Abq41560 Oligonucle	362	16.4	58.6	1365	3	ACA49046	Aca49046 Arabidops
c 290	16.6	59.3	1223	6	ABQ44567	Abq44567 Oligonucle	c 363	16.4	58.6	1404	4	AAI58819	Aai58819 Human pol
c 291	16.6	59.3	1223	6	ABQ44566	Abq44566 Oligonucle	c 364	16.4	58.6	1404	5	ADQ99040	Adq99040 DNA encod
c 292	16.6	59.3	1275	8	ADA70826	Ada70826 Rice gene	c 365	16.4	58.6	1404	9	ADB48800	AdB48800 Novel hum
c 293	16.6	59.3	1579	4	ABL01941	Ab101941 Drosophil	366	16.4	58.6	1455	5	AAH67851	Aah67851 C glutami
c 294	16.6	59.3	1584	8	ACA23970	AcA23970 Prokaryot	367	16.4	58.6	1473	2	AAQ91585	Aaq91585 Porphorym
c 295	16.6	59.3	1704	13	ADS58889	AdS58889 Bacterial	368	16.4	58.6	1496	2	AAQ07326	Aaq07326 Arabidops
c 296	16.6	59.3	1731	4	ABL08345	Ab108345 Drosophil	c 369	16.4	58.6	1513	4	AAQ41001	Aaq41001 cDNA enco
c 297	16.6	59.3	1974	13	ADT42349	Adt42349 Bacterial	c 370	16.4	58.6	1546	4	AAF71762	Aaf71762 Corynebac
c 298	16.6	59.3	2000	12	ADJ41159	Adj41159 plant cDN	371	16.4	58.6	1578	4	AAF71761	Aaf71761 Corynebac
c 299	16.6	59.3	2558	2	AAV35514	Aav35514 DNA encod	372	16.4	58.6	1578	6	ABG53556	Abg53556 DNA encod
c 300	16.6	59.3	2666	9	ADB84031	AdB84031 Japanese	373	16.4	58.6	1579	4	AAA89277	Aaa89277 Arabidops
c 301	16.6	59.3	2860	10	ADC37168	Adc37168 Nuclear f	374	16.4	58.6	1623	3	ACA49050	Aca49050 Arabidops
c 302	16.6	59.3	3636	4	AAAS1642	Aas1642 Staphyloc	375	16.4	58.6	1626	3	AAQ37639	Aaq37639 Arabidops
c 303	16.6	59.3	3697	4	ABL01940	Ab101940 Drosophil	376	16.4	58.6	1677	9	ADB09439	AdB09439 Alloiooc
c 304	16.6	59.3	3793	4	ABL08344	Ab108344 Drosophil	377	16.4	58.6	1754	3	AAAS3743	Aas3743 Plant tra
c 305	16.6	59.3	4437	8	ACF73516	Acf73516 Staphyloc	378	16.4	58.6	2369	6	ABK15556	Abk15556 DNA encod
c 306	16.6	59.3	4449	4	AAAS4749	Aas4749 Staphyloc	379	16.4	58.6	2748	12	ADM57406	AdM57406 F gondii
c 307	16.6	59.3	4585	4	ABL28758	Ab128758 Drosophil	380	16.4	58.6	3010	6	AAI48965	Aai48965 C glutami
c 308	16.6	59.3	4594	2	AAI13167	Aai13167 Enterococ	c 381	16.4	58.6	3040	4	AAH54425	Aah54425 S. epider
c 309	16.6	59.3	4594	6	ABS98962	AbS98962 Enterococ	c 382	16.4	58.6	3050	8	ABZ10011	Abz10011 Haematopo
c 310	16.6	59.3	5148	8	ADA68320	Ada68320 Arabidops	c 383	16.4	58.6	3050	13	ADS89359	AdS89359 Oligonucle
c 311	16.6	59.3	9372	10	ADD15194	AdD15194 Human DFF	c 384	16.4	58.6	3128	11	ACN88838	AcN88838 Breast ca
c 312	16.6	59.3	9372	12	ADM33394	AdM33394 Human PRO	385	16.4	58.6	3187	5	AAH88889	Aah88889 DNA encod

c 386	16.4	58.6	3870	8	ABZ42676	Abz42676 Human his	c 459	16.2	57.9	730	3	AAZ80609	Aaz80609 Human col
c 387	16.4	58.6	4008	12	ADL12429	Adl12429 Human etc	c 460	16.2	57.9	885	8	ACA53118	Acas3118 Prokaryot
c 388	16.4	58.6	4057	4	AH54243	Aah54243 S. epider	c 461	16.2	57.9	984	8	ACA51543	Acas1543 Prokaryot
c 389	16.4	58.6	4154	10	ADD47133	Add47133 Human gen	c 462	16.2	57.9	989	8	ACA48835	Acas4835 Prokaryot
c 390	16.4	58.6	4242	4	ABL05330	Ab105330 Drosophil	c 463	16.2	57.9	1056	4	AAD05228	Aad05228 Human sec
c 391	16.4	58.6	4270	4	ABL08659	Ab108659 Drosophil	c 464	16.2	57.9	1089	4	AAS44619	Aas44619 Human ful
c 392	16.4	58.6	4307	13	ACN42409	Acn42409 Human dia	c 465	16.2	57.9	1091	4	AAS44791	Aas44791 Human con
c 393	16.4	58.6	4329	13	ACN42407	Acn42407 Human dia	c 466	16.2	57.9	1112	6	ABQ42887	Abq42887 Oligonuc1
c 394	16.4	58.6	4321	13	ACN42408	Acn42408 Human dia	c 467	16.2	57.9	1112	6	ABQ42886	Abq42886 Oligonuc1
c 395	16.4	58.6	4580	4	ABL12621	Ab112621 Drosophil	c 468	16.2	57.9	1194	5	ADL63507	Adl63507 Human ova
c 396	16.4	58.6	4848	6	ABQ70991	Abq70991 Listeria	c 469	16.2	57.9	1225	3	ACA54094	Acas4094 Arabidops
c 397	16.4	58.6	5401	4	ABL11443	Ab111443 Drosophil	c 470	16.2	57.9	1232	3	ACA37247	Acac37247 Arabidops
c 398	16.4	58.6	5768	10	ADES9601	Ades9601 Human gen	c 471	16.2	57.9	1232	3	ACA37247	Acac37247 Arabidops
c 399	16.4	58.6	5856	10	ACF63378	Acf63378 Human his	c 472	16.2	57.9	1299	6	ABZ14542	Abz14542 Arabidops
c 400	16.4	58.6	5994	6	ABL32879	Ab132879 Human imm	c 473	16.2	57.9	1299	6	ADA68548	Ada68548 Arabidops
c 401	16.4	58.6	6050	4	AAS46791	Aas46791 Tumour su	c 474	16.2	57.9	1299	12	ADN74748	Adn74748 Thale Cre
c 402	16.4	58.6	6050	6	ABL34128	Ab134128 Human imm	c 475	16.2	57.9	1304	8	ABQ83878	Abq83878 Human MDD
c 403	16.4	58.6	6050	6	ABL34128	Ab134128 Human imm	c 476	16.2	57.9	1308	4	AAL04369	Aal04369 Human rep
c 404	16.4	58.6	6050	6	ABK33936	Abk33936 Human DNA	c 477	16.2	57.9	1454	3	AAC54201	Aac54201 Arabidops
c 405	16.4	58.6	6050	8	ADA20384	Ada20384 Prostate	c 478	16.2	57.9	1457	3	AAC53243	Aac53243 Arabidops
c 406	16.4	58.6	6050	8	ADA84191	Ada84191 Human ren	c 479	16.2	57.9	1540	10	ADF82111	Adf82111 Leukaemia
c 407	16.4	58.6	6050	10	ADER4105	Ades4105 Human lym	c 480	16.2	57.9	1643	10	ADA52947	Ada52947 Human cod
c 408	16.4	58.6	6235	6	ABL32786	Ab132786 Human imm	c 481	16.2	57.9	2000	12	ADJ40978	Adj40978 Plant CDN
c 409	16.4	58.6	6567	4	ABL08658	Ab108658 Drosophil	c 482	16.2	57.9	2004	5	AAS75921	Aas75921 Human ATP
c 410	16.4	58.6	6580	4	ABL12620	Ab112620 Drosophil	c 483	16.2	57.9	2311	5	AAS75921	Aas75921 DNA encod
c 411	16.4	58.6	7106	13	ADT05458	Adt05458 Haemophil	c 484	16.2	57.9	2715	13	ADS48830	Ades48830 Bacterial
c 412	16.4	58.6	7309	6	AAS46567	Aas46567 Tumour su	c 485	16.2	57.9	2733	10	ADE55479	Ades5479 Rat gene
c 413	16.4	58.6	7309	6	ABL33816	Ab133816 Human imm	c 486	16.2	57.9	2733	10	ADE55475	Ades5475 Rat gene
c 414	16.4	58.6	7309	10	ADB54163	Adb54163 Pretreat	c 487	16.2	57.9	2733	10	ADE55487	Ades5487 Rat gene
c 415	16.4	58.6	7309	13	ADBS9317	Adbs9317 Oligonuc1	c 488	16.2	57.9	2733	10	ADE55483	Ades5483 Rat gene
c 416	16.4	58.6	7611	4	ABL11442	Ab111442 Drosophil	c 489	16.2	57.9	3450	4	AAA91119	Aaa91119 Apaf-1XL
c 417	16.4	58.6	9474	6	ABK50462	Abk50462 Human his	c 490	16.2	57.9	3618	4	AAA91116	Aaa91116 Apaf-1L c
c 418	16.4	58.6	13606	4	AAS45458	Aas45458 Chemicall	c 491	16.2	57.9	3635	12	ADM86936	Adm86936 Human pro
c 419	16.4	58.6	13606	4	AAS45458	Aas45458 Chemicall	c 492	16.2	57.9	3710	10	ADE55485	Ades5485 Human gen
c 420	16.4	58.6	13606	4	ABL33811	Ab133811 Human imm	c 493	16.2	57.9	3710	10	ADE55481	Ades5481 Human gen
c 421	16.4	58.6	13606	6	ABK28314	Abk28314 DNA trans	c 494	16.2	57.9	3710	10	ADE55489	Ades5489 Human gen
c 422	16.4	58.6	18167	4	ABL06096	Ab106096 Drosophil	c 495	16.2	57.9	3714	4	AAA91117	Aaa91117 Apaf-1WD
c 423	16.4	58.6	84707	6	ABQ67196	Abq67196 6	c 496	16.2	57.9	3747	4	AAA91122	Aaa91122 Apaf-1XL
c 424	16.4	58.6	100608	13	ABD32769	Abd32769 Human can	c 497	16.2	57.9	3747	4	AAA91120	Aaa91120 Apaf-1XL
c 425	16.4	58.6	110000	6	ABQ69245	Abq69245 26	c 498	16.2	57.9	3747	4	AAA91118	Aaa91118 Apaf-1XL
c 426	16.4	58.6	110000	8	AAD53224	Aad53224 1	c 499	16.2	57.9	3747	4	AAA91125	Aaa91125 Apaf-1XL
c 427	16.4	58.6	110000	9	ADB12064	Adb12064 08	c 500	16.2	57.9	3747	4	AAA91124	Aaa91124 Apaf-1XL
c 428	16.4	58.6	110000	10	ADF77343	Adf77343 17							
c 429	16.4	58.6	110000	11	ACN43998	Acn43998 2							
c 430	16.4	58.6	175590	10	ADD50650	Add50650 BAC seque							
c 431	16.4	58.6	349980	5	AAS68525	Aas68525 C glutami							
c 432	16.4	58.6	349980	5	AAS68525	Aas68525 C glutami							
c 433	16.4	58.6	349980	5	AAS68533	Aas68533 C glutami							
c 434	16.2	57.9	299	6	ABK54748	Abk54748 Human col							
c 435	16.2	57.9	434	9	ACH21812	Ach21812 Human adu							
c 436	16.2	57.9	457	8	ABZ54905	Abz54905 Aspergill							
c 437	16.2	57.9	492	5	ADL44430	Adl44430 Human ova							
c 438	16.2	57.9	493	3	AAA06669	Aaa06669 Human imm							
c 439	16.2	57.9	493	4	AAS93785	Aas93785 Human pro							
c 440	16.2	57.9	493	4	AAS63878	Aas63878 Human pro							
c 441	16.2	57.9	493	4	RAH02850	Aah02850 Prostate							
c 442	16.2	57.9	493	4	AAS85099	Aas85099 Human pro							
c 443	16.2	57.9	493	5	ACA59686	Acas59686 Prostate							
c 444	16.2	57.9	493	6	ABL95249	Ab195249 Human 236							
c 445	16.2	57.9	493	8	ACC95413	Acc95413 Prostate							
c 446	16.2	57.9	493	10	ADB13900	Adb13900 Human pro							
c 447	16.2	57.9	493	10	ADG36316	Adg36316 Human pro							
c 448	16.2	57.9	509	3	ACA37295	Acac37295 Arabidops							
c 449	16.2	57.9	525	6	ABV87129	Abv87129 Human col							
c 450	16.2	57.9	538	12	ACH71924	Ach71924 Human gen							
c 451	16.2	57.9	539	10	ADG38307	Adg38307 Aspergill							
c 452	16.2	57.9	559	6	ABV87210	Abv87210 Human col							
c 453	16.2	57.9	613	6	ABN64627	Abn64627 Human can							
c 454	16.2	57.9	623	6	ABV89076	Abv89076 Human col							
c 455	16.2	57.9	644	3	AAP12943	Aap12943 Aspergill							
c 456	16.2	57.9	657	5	ADL38046	Adl38046 Human ova							
c 457	16.2	57.9	657	5	ADI72908	Adi72908 Human ova							
c 458	16.2	57.9	693	3	AAA78465	Aaa78465 Plant SDF							

ALIGNMENTS

RESULT 1

ABX15698	
ID	ABX15698 standard; DNA; 28 BP.
XX	
AC	ABX15698;
XX	
DT	31-MAR-2003 (first entry)
XX	
DE	Dengue virus detection PCR primer #2.
XX	
XX	PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;
KW	dengue haemorrhagic fever; virus; viral detection.
OS	Dengue virus.
XX	
EN	US2002155435-A1.
XX	
PD	24-OCT-2002.
XX	
PF	28-FEB-2002; 2002US-00085944.
XX	
PR	01-MAR-2001; 2001US-0272535P.
XX	
PA	(WANG/) WANG W.
XX	
PI	Wang W;

XX WPI; 2003-182625/18.

XX New dengue virus-specific primers, useful for reverse transcriptase-
PT polymerase chain reaction assays, particularly for detecting or
PT quantitating dengue virus in a sample.

XX Claim 28; Page 1; 6pp; English.

XX This invention relates to novel Dengue virus reverse transcriptase (RT)
XX PCR primers which may be used to detect Dengue virus in a sample. Dengue
CC virus is a member of the flavivirus family and causes diseases including
CC dengue fever (DF) and dengue haemorrhagic fever. The invention also
CC comprises a method for detecting and quantitating dengue virus. The
CC dengue virus-specific primers of the invention are useful in reverse
CC transcriptase-polymerase chain reaction assays, particularly for
CC detecting or quantitating dengue virus in a sample. The present sequence
CC represents a dengue virus specific RT-PCR primer used in the method of
CC the invention

XX SQ Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 1 AATATGCTGAACGCGAGAGAAACCGCG 28

RESULT 2
ADR47007
ID ADR47007 standard; DNA; 2328 BP.

XX AC ADR47007;

XX 18-NOV-2004 (first entry)

XX Dengue virus DNA for vaccine.

DE ds; gene; cytostatic; virucide; dengue virus; recombinant replicon;
KW deletion; preM protein; C protein; NS1 protein signal; vaccine;
KW cervical cancer; viral disease; antigen; dendritic cell; immune response;
KW human papillomavirus.

XX Dengue virus.

OS WO2004072274-A1.

XX 26-AUG-2004.

XX 30-JAN-2004; 2004WO-CN000088.

XX 30-JAN-2003; 2003CN-00115272.

XX 30-JAN-2003; 2003CN-00115273.

XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA (TENG-) TENGGEN BIOMEDICAL CO.
PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX Pang X;

XX WPI; 2004-625870/60.

XX Virus-like particle vaccines containing dengue virus recombinant replicon
PT as core for carrier, applicable in preventives or/and remedies for tumors
PT like cervical cancer and viral diseases.

XX Claim 3; SEQ ID NO 4; 38pp; Chinese.

XX A dengue virus recombinant replicon has a deletion of the complete coding
CC sequence for preM protein of dengue virus and also includes elements of

CC e.g. the non-coding region in the whole of the 5'-end, the coding region
CC of the front 20 amino acids in the C protein, and the coding region of
CC NS1 protein signal; coding regions of all non-structural proteins. The
CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to a Dengue virus DNA sequence used in
CC the recombinant replicon of the invention.

XX SQ Sequence 2328 BP; 775 A; 468 C; 585 G; 500 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 13; Length 2328;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 3
ABX13740
ID ABX13740 standard; DNA; 2357 BP.

XX AC ABX13740;

XX 28-FEB-2003 (first entry)

XX Dengue virus type 2 structural gene genome segment.

DE Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;
KW preM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;
KW mosquito; Aedes aegyptii; acute undifferentiated fever;
KW dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS;
KW immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
KW structural gene; virucide.

XX Dengue virus.

OS US6455509-B1.

XX 24-SEP-2002.

XX 04-JUN-1997; 97US-00869423.

XX 04-JUN-1996; 96US-0017839P.

XX (USNA) US SEC OF NAVY.

XX Kocheil TJ, Porter XR, Raviprakash K, Hoffman SL, Hayes CG;
XX WPI; 2003-066244/06.

XX New pharmaceutical compositions containing dengue nucleic acids, useful
PT as a vaccine, particularly for inducing a protective immune response in
PT mammalian subjects against the dengue virus infection.

XX Disclosure; Col 17-20; 26pp; English.

XX The invention discloses a pharmaceutical composition capable of inducing
CC an immune response in a mammalian subject, comprising an immunogenic
CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
CC which includes the envelope and membrane (preM) genes of a dengue type 1,
CC 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of
CC the family Flaviviridae and is a positive strand RNA virus encoding ten

CC proteins. These genes are translated as a polypeptide which is cleaved by
 CC host and viral proteases. The virus envelope protein is a major antigen
 CC which can be targeted by neutralising antibodies. The membrane protein
 CC also appears on the virion surface and is required for proper processing
 CC of the envelope protein. Dengue viruses are transmitted primarily by the
 CC mosquito, *Aedes aegypti*, and can lead to human illnesses ranging from
 CC acute febrile illness to dengue haemorrhagic fever (DHF) and
 CC dengue shock syndrome (DSS). Secondary infections, with a different
 CC serotype, may lead to an immune enhancement phenomenon. The compositions
 CC of the invention are DNA vaccines which are injected into the animal as a
 CC technique of gene therapy. The composition is useful as a vaccine,
 CC particularly for inducing a protective immune response in mammalian
 CC subjects against the dengue virus infection. The sequence presented is
 CC the dengue virus type 2 (Den 2) structural gene genome segment
 XX
 SQ Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 8; Length 2357;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 Db 60 AATATGCTGAACCGGAGAGAAACCGCG 87

RESULT 4
 ADG93319
 ID ADG93319 standard; DNA; 2423 BP.
 XX
 AC ADG93319;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.

XX immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
 KW dengue type 4; virucide; immunostimulant; vaccine; tetra-valent vaccine;
 KW dengue virus; delta30; attenuating mutation; humoral response;
 KW cellular response; non-structural protein; structural protein;
 KW dengue virus serotype; gene; ds; plasmid P2.

XX Dengue virus type 1.
 XX WO2003092592-A2.
 XX 13-NOV-2003.

XX 25-APR-2003; 2003WO-US013279.
 XX
 XX 03-MAY-2002; 2002US-0377860P.
 XX 23-DEC-2002; 2002US-0436500P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
 XX Hanley K;
 XX WPI; 2004-022612/02.
 XX P-PSDB; ADG93320.

XX New tetra-valent vaccine containing a common nucleotide deletion in the 3'
 PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
 FT of disease in humans caused by dengue virus, or for inducing immune
 PT response.

XX Disclosure; SEQ ID NO 52; 181pp; English.

XX This invention relates to a novel immunogenic composition being
 CC tetra-valent and containing a common nucleotide deletion in the 3'
 CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
 CC useful for the development of compounds with a virucide or
 CC immunostimulant activity or as a vaccine. The tetra-valent vaccine is

CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetra-valent vaccine, the new tetra-valent vaccine is
 CC unique since they contain a common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta30 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC) structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN1 ME chimeric region DNA which is related to
 CC the invention.

SQ Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 2423;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 Db 138 AATATGCTGAACCGGAGAGAAACCGCG 165

RESULT 5
 AAT47666
 ID AAT47666 standard; cDNA; 3381 BP.

XX AAT47666;
 XX
 DT 17-OCT-2003 (revised)
 DT 19-MAY-1997 (first entry)
 XX
 DE Dengue virus serotype 2 PR159/S1 mutant sequence.
 XX DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.

XX Dengue virus; serotype 2.

XX Key Location/Qualifiers
 FT mutation 1216..1218
 FT /*tag= a
 FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
 FT is GAA (Glu) in wild-type PR159"
 FT mutation 1258..1260
 FT /*tag= b
 FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1
 FT is GTG (Val) in wild-type PR159"
 FT mutation 1762..1764
 FT /*tag= c
 FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
 FT is ATT (Ile) in wild-type PR159"
 FT mutation 1927..1929
 FT /*tag= d
 FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
 FT is AGT (Ser) in wild-type PR159"

XX WO9637221-A1.

XX 28-NOV-1996.

XX 24-MAY-1996; 96WO-US007627.

XX 24-MAY-1995; 95US-00448734.

XX 07-JUN-1995; 95US-00488807.

XX 10-JUL-1995; 95US-00500469.

XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Nakano E, Clements D;

XX WPI; 1997-020938/02.

XX P-PSDB; AAW09409.

XX Sub:unit vaccine against flavivirus infection - contg. recombinant

PT envelope protein in secretible form, used for immunising against
PT flavivirus infection.

PS Example 1; Fig 3A-D; 121pp; English.

XX A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
CC conservative mutation in domain B of S1 that may be involved in the
CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of
CC the virus. The clone can be used to express recombinant secreted
CC polypeptides, comprising portions of the envelope protein (esp. domain B,
CC Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and
CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
CC infection. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 3381;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAGAAACCGCG 28

DB 40 AATATGCTGAACGCGGAGAGAAACCGCG 67

RESULT 6

AAAX25114

ID AAX25114 standard; cDNA; 3381 BP.

AC AAX25114;

XX 17-OCT-2003 (revised)

DT 05-JUL-1999 (first entry)

XX Dengue virus serotype 2 PR159/S1 viral capsid, prM, E, NS1 cDNA.

XX Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.

XX Dengue virus; serotype 2.

XX WO9906068-A2.

XX 11-FEB-1999.

XX 27-JUL-1998; 98WO-US015447.

XX 31-JUL-1997; 97US-00904227.

XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.

XX Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KB;

XX WPI; 1999-153454/13.

XX P-PSDB; AAY05522.

XX Recombinant dimeric flavivirus envelope vaccine - comprising a dimeric
PT 80% E protein, useful for protecting against flavivirus, especially dengue
PT virus infections.

XX Example 1; Fig 3A-D; 60pp; English.

XX This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
CC (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
CC strain served as the source for DEN-2 genes used in the invention. A
CC vaccine for protecting against flavivirus infection comprises a dimeric
CC 80% E protein that has been secreted as a recombinant protein from a
CC eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
CC The dimeric truncated E is formed: (1) by directly linking 2 tandem
CC copies of 80% E via a flexible tether; (2) via the formation of a leucine
CC zipper domain through the homodimeric association of 2 leucine zipper
CC helices each fused to the C-terminus of an 80% E molecule; or (3) via the

CC formation of a non-covalently associated four-helix bundle domain formed
CC upon association of two helix-turn-helix moieties attached to the C-
CC terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
CC efficiently secreted by recombinant cells, are easier to purify than
CC intracellular proteins, and generate a high titer neutralising antibody
CC response. The method is generally applicable to flaviviruses, in
CC particular dengue viruses such as DEN-2, where 80% E comprises amino
CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
CC infection. (Updated on 17-OCT-2003 to standardise OS field)

XX SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 3381;

Best Local Similarity 100.0%; Pred. No. 0.013;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAGAAACCGCG 28

DB 40 AATATGCTGAACGCGGAGAGAAACCGCG 67

RESULT 7

ADL98085

ID ADL98085 standard; DNA; 3381 BP.

XX ADL98085;

XX 18-NOV-2004 (first entry)

XX Dengue virus, DEN-2, partial genome.

XX Dengue virus; DEN-2; ss; Envelope protein; 80% E; membrane protein;

XX capsid protein; NS1 protein; Dengue haemorrhagic fever; DHF;

XX Dengue shock syndrome; DSS; flavivirus; vaccine.

XX Dengue virus type 2; strain PR159/S1.

XX Key Location/Qualifiers

FT CDS 1..3381

FT /*tag= a

FT /product= "DEN-2 Capsid-membrane-envelope-NS1 proteins"

FT /partial

FT /note= "No stop codon shown"

XX US2003175304-A1.

XX 18-SEP-2003.

XX 20-SEP-2002; 2002US-00247960.

XX 31-JUL-1997; 97US-00904227.

XX 18-AUG-1999; 99US-00376463.

XX (PETE/) PETERS I D.

XX (COLL/) COLLIER B G.

XX (MCDO/) MCDONELL M.

XX (IVYJ/) IVY J M.

XX (HARA/) HARADA K.

XX Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;

XX WPI; 2003-898503/82.

XX P-PSDB; ADL98086.

XX Vaccine useful for protection against dengue virus infection, comprises a
PT dimeric 80% envelope, which has been secreted as a recombinantly produced
PT protein from Drosophila Schneider cells.

XX Example 1; Fig 3; 31pp; English.

XX The invention relates to a vaccine for protection against flavivirus
CC infection comprising a dimeric 80% envelope (E), which has been secreted
CC as a recombinantly produced protein from Drosophila Schneider cells and

CC which represents the N-terminal 80% portion of the protein from residue 1
 CC -395. Also included are a method for protecting a subject against a
 CC Flavivirus, an immunogenic polypeptide comprising a dimeric 80% E, an
 CC immunogenic composition for protection against Flavivirus infection
 CC comprising the immunogenic polypeptide and a carrier, an immunodiagnostic
 CC for detecting Flavivirus comprising the immunogenic polypeptide, a vector
 CC host recombinant DNA expression system, a DNA sequence encoding the
 CC immunogenic polypeptide and an immunodiagnostic kit for detecting
 CC Flavivirus in a test subject. The dimeric 80% E products are envelope
 CC proteins of serotypes comprising DEN-1, DEN-2, DEN-3 or DEN-4. The
 CC Flavivirus is a dengue virus. The 80% E protein is produced as a dimer by
 CC incorporating 2 different kinds of leucine zipper peptides or
 CC incorporating a helix-turn-helix peptide, to encourage dimerization. The
 CC vaccine is useful for protection against dengue virus infection (e.g.
 CC Dengue haemorrhagic fever, DHF, and Dengue shock syndrome, DSS). The
 CC present sequence is the partial genomic sequence of the DEN-2 strain
 CC PR159/S1 virus, encoding the capsid, membrane, envelope and NS1 proteins.
 XX
 SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 11; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 8

ADQ28715
 ID ADQ28715 standard; DNA; 3381 BP.

AC ADQ28715;

XX 26-AUG-2004 (first entry)

XX Dengue virus viral capsid, prM, E and NS1 genes.

XX virucide; vaccine; Flavivirus; dimeric 80%E; Drosophila Schneider cell;
 KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
 KW viral capsid; prM gene; E gene; NS1 gene; da.

XX Dengue virus.

Key	Location/Qualifiers
FT CDS	1..3381
FT	/*tag= a
FT	/product= "Dengue virus viral capsid, prM, E and NS1 polypeptide"

XX US6749857-B1.

XX 15-JUN-2004.

XX 18-AUG-1999; 99US-00376463.

XX 31-JUL-1997; 97US-00904227.

XX (HAWAII) HAWAII BIOTECHNOLOGY GROUP INC.

XX Peters ID, Coller BG, McDonnell M, Ivy JM, Harada K;

XX WPI; 2004-438725/41.

DR P-PSDB; ADQ28716.

XX New vaccines for preventing or diagnosing infections caused by dengue
 PT virus comprises a therapeutic amount of a dimeric 80%E protein secreted
 PT from Drosophila Schneider cells.

XX Example 1; SEQ ID NO 2; 47pp; English.

XX The invention describes a vaccine that generates a protective,

CC neutralising antibody response to a Flavivirus in a murine host. The
 CC vaccine comprises a therapeutic amount of a dimeric 80%E, the dimeric
 CC 80%E having been secreted as a recombinantly produced protein from
 CC Drosophila Schneider cells, and where 80%E represents the N-terminal 80%
 CC portion of the protein from residues 1-395. Also described are: an
 CC immunogenic polypeptide comprising the dimeric 80%E cited above; an
 CC immunogenic composition that generates a protective, neutralising
 CC antibody response to a Flavivirus in a murine host, comprising the above
 CC immunogenic polypeptide and a physiological carrier; a multivalent
 CC immunodiagnostic for the detection of Flavivirus, comprising at least 2
 CC of the above immunogenic polypeptides of at least 2 flavivirus serotypes;
 CC and an immunodiagnostic kit for the detection of Flavivirus in a test
 CC subject, comprising the above immunogenic or multivalent immunodiagnostic
 CC polypeptide, a suitable support phase coated with dimeric 80%E, and
 CC labeled antibodies immunoreactive to antibodies from the test subject.
 CC The composition is useful for preventing or diagnosing infections caused
 CC by dengue virus. This sequence encodes Dengue virus gene viral capsid,
 CC prM, E and NS1 genes for Dengue virus strain PR159/S1 used as the source
 CC of DEN-2 genes for the invention.
 XX

SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 9

AD53912

ID AD53912 standard; DNA; 10616 BP.

XX AD53912;

XX 28-MAY-2003 (first entry)

XX Dengue virus type 2 strain rDEN2/4delta30 DNA.

XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; da.

XX Dengue virus.

Key	Location/Qualifiers
FT CDS	97..10263
FT	/*tag= a
FT	/product= "DEN4 strain rDEN2/4delta30 protein"
FT mat_peptide	97..438
FT	/*tag= c
FT	/product= "Anchored capsid protein"
FT mat_peptide	97..396
FT	/*tag= b
FT	/product= "Virion capsid protein"
FT mat_peptide	439..936
FT	/*tag= d
FT	/product= "Membrane precursor protein"
FT mat_peptide	712..936
FT	/*tag= e
FT	/product= "Membrane protein"
FT mat_peptide	937..2421
FT	/*tag= f
FT	/product= "Envelope protein"
FT mat_peptide	2422..3477
FT	/*tag= g
FT	/product= "NS1 protein"
FT mat_peptide	3478..4131
FT	/*tag= h
FT	/product= "NS2A protein"
FT mat_peptide	4132..4521
FT	/*tag= i
FT	/product= "NS2B protein"

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FT mat_peptide 4522..6375
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide 6376..6756
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide 6757..6825
FT /*tag= l
FT /product= "2K protein"
FT mat_peptide 6826..7560
FT /*tag= m
FT /product= "NS4B protein"
FT mat_peptide 7561..10260
FT /*tag= n
FT /product= "NS5 protein"
XX
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX characteristics of dengue virus vaccines for the prevention and/or
XX treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
XX phenotype in which the viral genome is modified by introduction of a
XX mutation, singly or in combination, taken from mutations from recombinant
XX virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX dengue type 4 virus. The methods and compositions of the invention are
XX useful for fine tuning the attenuation and growth characteristics of
XX dengue virus vaccines for the prevention and/or treatment of dengue virus
XX infection. The present sequence is Dengue virus type 4 strain
XX rDEN2/4delta30 DNA
XX
XX Query Match 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
XX Best Local Similarity 100.0%; Score 28; DB 10; Length 10616;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||||
XX 136 AATATGCTGAACCGGAGAGAAACCGCG 163
XX
XX RESULT 10
XX AAD14612
XX ID AAD14612 standard; cDNA; 10648 BP.
XX
XX AC AAD14612;
XX
XX 11-SEP-2003 (revised)
XX 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-4 1036 cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX mat_peptide 4522..6375
XX /*tag= j
XX /product= "NS3 protein"
XX mat_peptide 6376..6756
XX /*tag= k
XX /product= "NS4A protein"
XX mat_peptide 6757..6825
XX /*tag= l
XX /product= "2K protein"
XX mat_peptide 6826..7560
XX /*tag= m
XX /product= "NS4B protein"
XX mat_peptide 7561..10260
XX /*tag= n
XX /product= "NS5 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07991.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 3; Page 373-389; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Query Match 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
XX Best Local Similarity 100.0%; Score 28; DB 4; Length 10648;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||||
XX 138 AATATGCTGAACCGGAGAGAAACCGCG 165
XX
XX RESULT 11
XX AAD14613
XX ID AAD14613 standard; cDNA; 10648 BP.
XX
XX AC AAD14613;
XX
XX 01-NOV-2001 (first entry)
XX
XX Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX ss.

```

XX Dengue virus; type IV.
OS Synthetic.
XX

XX Key Location/Qualifiers
FT CDS 102..10265
FT /*tag= a
FT /product= "DEN-4 PDK-48 protein variant"
FT replace(1211, T)
FT /*tag= b
FT mutation replace(1971, G)
FT /*tag= c
FT mutation replace(3182, G)
FT /*tag= d
FT mutation replace(6660, C)
FT /*tag= e
FT mutation replace(6957, A)
FT /*tag= f
FT mutation replace(7162, T)
FT /*tag= g
FT mutation replace(7546, C)
FT /*tag= h
FT mutation replace(7623, G)
FT /*tag= i

XX WO200160847-A2.
XX
XX
XX
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07992.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 4; Page 397-413; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. DEN-4 virus passaged in primary dog kidney (PDK) cells
XX 48 times is designated as DEN-4 PDK-48 virus
XX
XX Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;

Query Match 100.08; Score 28; DB 4; Length 10648;
Best Local Similarity 100.08; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165

RESULT 12
AADS3911
ID AADS3911 standard; DNA; 10649 BP.
XX
XX AADS3911;
XX
XX 28-MAY-2003 (first entry)
XX Recombinant dengue virus type 4 strain rDEN4 DNA.
XX
XX Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; da.
XX Dengue virus.
XX
XX Key Location/Qualifiers
FT CDS 102..10649
FT /*tag= a
FT /product= "DEN4 strain rDEN4 protein"
FT mat_peptide 102..440
FT /*tag= c
FT /product= "Anchored capsid protein"
FT mat_peptide 102..398
FT /*tag= b
FT /product= "Virion capsid protein"
FT mat_peptide 441..938
FT /*tag= d
FT /product= "Membrane precursor protein"
FT mat_peptide 714..938
FT /*tag= e
FT /product= "Membrane protein"
FT mat_peptide 939..2423
FT /*tag= f
FT /product= "Envelope protein"
FT mat_peptide 2424..3479
FT /*tag= g
FT /product= "NS1 protein"
FT mat_peptide 3480..4133
FT /*tag= h
FT /product= "NS2A protein"
FT mat_peptide 4134..4523
FT /*tag= i
FT /product= "NS2B protein"
FT mat_peptide 4524..6377
FT /*tag= j
FT /product= "NS3 protein"
FT mat_peptide 6378..6758
FT /*tag= k
FT /product= "NS4A protein"
FT mat_peptide 6638..7562
FT /*tag= m
FT /product= "NS4B protein"
FT mat_peptide 6759..6827
FT /*tag= l
FT /product= "2K protein"
FT mat_peptide 7563..10262
FT /*tag= n
FT /product= "NS5 protein"
XX WO200295075-A1.
XX
XX 28-NOV-2002.
XX
XX 22-MAY-2002; 2002WO-US016308.
XX
XX 22-MAY-2001; 2001US-0293049P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX

```
XX PI Whitehead SS, Murphy BR, Hanley KA;
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35313.
XX PT New mutated flavivirus, useful for fine tuning the attenuation and growth
XX PT characteristics of dengue virus vaccines for the prevention and/or
XX PT treatment of dengue virus infection.
XX PS Disclosure; Page 131-132; 246pp; English.
XX SS The present invention relates to novel mutated flaviviruses comprising a
XX CC phenotype in which the viral genome is modified by introduction of a
XX CC mutation, singly or in combination, taken from mutations from recombinant
XX CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX CC dengue type 4 virus. The methods and compositions of the invention are
XX CC useful for fine tuning the attenuation and growth characteristics of
XX CC dengue virus vaccines for the prevention and/or treatment of dengue virus
XX CC infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
XX SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 10; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
RESULT 13
ID AAD53910
XX AAD53910 standard; DNA; 10649 BP.
XX AC AAD53910;
XX DT 28-MAY-2003 (first entry)
XX DE Dengue virus type 4 strain 2A DNA.
XX KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds..
XX OS Dengue virus.
XX PH Key Location/Qualifiers
XX FT CDS 102..10649
FT /*tag= a
FT /*product= "DEN4 strain 2A protein"
FT mat_peptide 102..440
FT /*tag= c
FT /*product= "Anchored capsid protein"
FT mat_peptide 102..398
FT /*tag= b
FT /*product= "Virion capsid protein"
FT mat_peptide 441..938
FT /*tag= d
FT /*product= "Membrane precursor protein"
FT mat_peptide 714..938
FT /*tag= e
FT /*product= "Membrane protein"
FT mat_peptide 939..2423
FT /*tag= f
FT /*product= "Envelope protein"
FT mat_peptide 2424..3479
FT /*tag= g
FT /*product= "NS1 protein"
FT mat_peptide 3480..4133
FT /*tag= h
FT /*product= "NS2A protein"
FT mat_peptide 4134..4523
```

```
FT /*tag= i
FT /*product= "NS2B protein"
FT mat_peptide 4524..6377
FT /*tag= j
FT /*product= "NS3 protein"
FT mat_peptide 6378..6758
FT /*tag= k
FT /*product= "NS4A protein"
FT mat_peptide 6759..6827
FT /*tag= l
FT /*product= "2K protein"
FT mat_peptide 6828..7562
FT /*tag= m
FT /*product= "NS4B protein"
FT mat_peptide 7563..10262
FT /*tag= n
FT /*product= "NS5 protein"
XX WO200295075-A1.
XX 28-NOV-2002.
XX 22-MAY-2002; 2002WO-US016308.
XX 22-MAY-2001; 2001US-0293049P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (BLAN/) BLANEY J E.
XX Whitehead SS, Murphy BR, Hanley KA;
XX WPI; 2003-120809/11.
XX P-PSDB; AAE35312.
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
XX PT characteristics of dengue virus vaccines for the prevention and/or
XX PT treatment of dengue virus infection.
XX PS Disclosure; Page 123-126; 246pp; English.
XX CC The present invention relates to novel mutated flaviviruses comprising a
XX CC phenotype in which the viral genome is modified by introduction of a
XX CC mutation, singly or in combination, taken from mutations from recombinant
XX CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
XX CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
XX CC dengue type 4 virus. The methods and compositions of the invention are
XX CC useful for fine tuning the attenuation and growth characteristics of
XX CC dengue virus vaccines for the prevention and/or treatment of dengue virus
XX CC infection. The present sequence is Dengue virus type 4 strain 2A DNA
XX SQ Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 10; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
RESULT 14
ID AAD14605
XX AAD14605 standard; cDNA; 10717 BP.
XX AC AAD14605;
XX DT 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX DE Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
```

KW immunogenic; viral disease; pharmaceutical; chimeric; ss.

OS Dengue virus; type II.

OS Dengue virus; type III.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 97..10266

FT /*tag= a

FT /product= "DEN-2/3-vp1 fusion protein"

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07984.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
FT vaccinating against a range of dengue viruses.

XX Example 2; Page 203-219; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present CDNA
CC sequence encodes dengue virus (DEN)-2/3-vp1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and from wild-
CC premenbrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 4; Length 10717;

XX Best Local Similarity 100.0%; Pred. No. 0.015;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 AATATGCTGAACCGCGAGAGAACCGCG 28

XX 136 AATATGCTGAACCGCGAGAGAACCGCG 163

XX RESULT 15

XX AAQ12787

XX ID AAQ12787 standard; RNA; 10723 BP.

XX XX

XX AAQ12787;

XX 25-MAR-2003 (revised)

XX 21-NOV-1991 (first entry)

XX Dengue 2 virus genome.

XX dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.

XX XX

OS Dengue virus.

XX Key

FT CDS

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

XX FR2654113-A.

XX 10-MAY-1991.

XX 09-NOV-1989; 89PR-00914724.

XX 09-NOV-1989; 89PR-00014724.

XX (INSP) INST PASTEUR.

XX Vincent D;

XX WPI; 1991-225002/31.

XX P-PSDB; AAR13166.

XX Detection and identification of Flaviviridae in biological sample - by

XX amplifying consensus sequence then hybridisation opt. followed by typing,

XX e.g. sequencing amplified prod.

XX Disclosure; Fig 3; 24pp; French.

XX The dengue 2 virus is an example of a member of the Flaviviridae which

XX can be identified using the probe pair of the invention. A species-

XX specific sequence can be amplified using the claimed oligonucleotides as

XX primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses

XX which can be identified include Japanese encephalitis virus and yellow

XX fever virus. (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;

XX Query Match 100.0%; Score 28; DB 2; Length 10723;

XX Best Local Similarity 89.3%; Pred. No. 0.015;

XX Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

XX 1 AATATGCTGAACCGCGAGAGAACCGCG 28

XX 136 AAUAGUCGUAACCGCGAGAGAACCGCG 163

XX RESULT 16


```

AAT49303
ID AAT49303 standard; cDNA; 10723 BP.
XX
AC AAT49303;
XX
27-AUG-2003 (revised)
DT 11-SEP-1997 (first entry)
DE
DE cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; SS.
XX
OS Dengue virus type 2 (strain 16681).
XX
FH Key Location/Qualifiers
FT 97..10272
FT /*tag= a
FT /product= "DEN-2 polyprotein
FT /transl_except(pos:9208..9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
XX
PN WO9640933-A1.
XX
PD 19-DEC-1996.
XX
PP 06-JUN-1996; 96WO-US009209.
XX
PR 07-JUN-1995; 95US-00483292.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
PI Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
DR WPI; 1997-052330/05.
DR P-PSDB; AAW06590.
XX
PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
PS Claim 23; Page 107-121; 261pp; English.
XX
CC This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3,
CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
CC -53, may be used in the production of a quadravalent vaccine which
CC provides immunity against all four serotypes of dengue virus. The vaccine
CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
CC protect against infection by all four serotypes of dengue virus, DEN-1,
CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
CC to produce the recombinant protein products of the DNA constructs which
CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;
Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

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RESULT 17

```

AAT49304
ID AAT49304 standard; cDNA; 10723 BP.
XX
AC AAT49304;
XX
27-AUG-2003 (revised)
DT 12-SEP-1997 (first entry)
DE
DE cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; SS.
XX
OS Dengue virus type 2 (strain 16681).
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 57
FT /*tag= b
FT /note= "C>T mutation"
FT 97..10272
FT /*tag= a
FT /product= "DEN-2 attenuated polyprotein
FT /transl_except(pos:643..645, aa:Xaa)
FT /transl_except(pos:1135..1137, aa:Xaa)
FT /transl_except(pos:1393..1395, aa:Xaa)
FT /transl_except(pos:2809..2811, aa:Xaa)
FT /transl_except(pos:3040..3042, aa:Xaa)
FT /transl_except(pos:9208..9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
FT 524
FT /*tag= c
FT /note= "A>T mutation, causes Asp to Val substitution"
FT 2055
FT /*tag= d
FT /note= "C>T mutation"
FT 2579
FT /*tag= e
FT /note= "G>A mutation, causes Gly to Asp substitution"
FT 4018
FT /*tag= f
FT /note= "C>T mutation, causes Leu to Phe substitution"
FT 5547
FT /*tag= g
FT /note= "C>T mutation"
FT 6599
FT /*tag= h
FT /note= "G>C mutation, causes Gly to Ala substitution"
FT 8571
FT /*tag= i
FT /note= "C>T mutation"
XX
WO9640933-A1.
XX
19-DEC-1996.
XX
06-JUN-1996; 96WO-US009209.
XX
07-JUN-1995; 95US-00483292.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
PI Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
DR WPI; 1997-052330/05.
DR P-PSDB; AAW06591.
XX
PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -

```

PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX This sequence encodes the polyprotein from an attenuated derivative of
CC Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
CC polyprotein comprises the capsid, pM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
CC NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
CC production of a quadravalent vaccine which provides immunity against all
CC four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
CC -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
CC The new quadravalent vaccines are used to protect against infection by
CC all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
CC can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
CC syndrome (DHF/DSS). Host cells are used to produce the recombinant
CC protein products of the DNA constructs which are used in the vaccines.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
XX
SQ Sequence 10723 BP; 3548 A; 2196 C; 2711 G; 2261 T; 0 U; 7 Other;

Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 18
AAD14614
ID AAD14614 standard; cDNA; 10723 BP.
XX
AC AAD14614;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/1-VP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type I.
OS Dengue virus; type II.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2/1-VP1 fusion protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07993.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 5; Page 422-438; 470pp; English.
XX

CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premembrane/membrane protein (pM) and an envelope protein (E) from wild-
CC type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGGAGAGAAACCGCG 163

RESULT 19
AAD14607
ID AAD14607 standard; cDNA; 10723 BP.
XX
AC AAD14607;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Wild-type, virulent DEN-2 16681 cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
OS Dengue virus; type II.
XX
FH Key Location/Qualifiers
FT CDS 97..10272
FT /*tag= a
FT /product= "DEN-2 16681 protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
DR WPI; 2001-497162/54.
DR P-PSDB; AAE07986.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 252-268; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural proteins of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC premembrane/membrane protein (pM) and an envelope protein (E) from wild-
CC type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;

CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
 CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
 CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
 CC contains 5' non-coding region followed by a capsid protein (C) encoding
 CC region, premembrane/membrane protein (prM) encoding region, an envelope
 CC protein (E) encoding region, followed by the region encoding non-
 CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163

RESULT 20

AAD14606
 ID AAD14606 standard; cDNA; 10723 BP.

XX
 AC AAD14606;

DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)

DE Dengue virus (DEN)-2/4-VPI chimeric cDNA.

KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.

OS Dengue virus; type II.
 OS Dengue virus; type IV.
 OS Chimeric.

XX Key Location/Qualifiers
 FT mutation 97..10272
 FT CDS /*tag= a

FT /*product= "DEN-2/4-VPI fusion protein"

FT WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

XX WPI; 2001-497162/54.

XX P-PSDB; AAE07985.

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.

XX Example 3; Page 227-243; 470pp; English.

XX The invention relates to avirulent, immunogenic flavivirus chimeras

CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes dengue virus (DEN)-2/4-VPI fusion protein related to the
 CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 CC comprising a valine at the non-structural protein (NS3)-250 and the
 CC premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
 |||||
 DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163

RESULT 21

AAD14608
 ID AAD14608 standard; cDNA; 10723 BP.

XX
 AC AAD14608;

DT 01-NOV-2001 (first entry)

DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.

KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.

OS Dengue virus; type II.
 OS Synthetic.

XX Key Location/Qualifiers
 FT mutation replace(57, C)
 FT /*tag= b

FT CDS 97..10272

FT /*tag= a

FT /*product= "DEN-2 PDK-53 protein variant"

FT mutation replace(524, A)

FT /*tag= c

FT mutation replace(2055, C)

FT /*tag= d

FT mutation replace(2579, G)

FT /*tag= e

FT mutation replace(4018, C)

FT /*tag= f

FT mutation replace(5270, A)

FT /*tag= g

FT mutation replace(5547, T)

FT /*tag= h

FT mutation replace(6599, G)

FT /*tag= i

FT mutation replace(8571, C)

FT /*tag= j

XX WO200160847-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005142.

XX 16-FEB-2000; 2000US-0182829P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX P-PSDB; AAE07987.
XX WPI; 2001-497162/54.
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX Example 1; Page 276-292; 470pp; English.
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present CDNA
XX sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region
XX
SQ Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGCGAGAGAAACCGCG 163
RESULT 22
ADN98025
ID ADN98025 standard; DNA; 10724 BP.
XX
XX AC ADN98025;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Dengue Virus isolate New Guinea complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX OS Dengue virus.
XX
XX PN WO2004040263-A2.
XX
XX PD 13-MAY-2004.
XX
XX PF 31-OCT-2003; 2003WO-US034823.
XX
XX PR 31-OCT-2002; 2002US-0422755P.
XX
XX PR 06-JUN-2003; 2003US-0476513P.
XX
XX PA (HEAL-) HEALTH RES INC.
XX

PI Wong SJ, Pei-Yong S;
XX WPI; 2004-400223/37.
XX
XX PT New diagnostic kit comprising West Nile Virus (WNV) envelope protein
XX reactive with antibody against WNV and cross-reactive with antibody
XX against a flavivirus, useful in diagnosing flavivirus infection caused by
XX DENV, WNV, JEV or SLEV.
XX
XX PS Disclosure; Fig 40; 212pp; English.
XX
XX CC The invention relates to a diagnostic kit comprising at least one
XX isolated and purified polypeptide comprising a West Nile Virus (WNV)
XX envelope (E) protein or its immunogenic fragment having a native
XX conformation or non-denatured structure and that is reactive with
XX antibodies against WNV and cross-reactive with antibodies against a
XX flavivirus. The diagnostic kit is useful in diagnosing flavivirus
XX infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
XX the complete nucleotide sequence of the DENV isolate New Guinea.
XX
SQ Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 12; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
|||||
Db 136 AATATGCTGAACCGCGAGAGAAACCGCG 163
RESULT 23
AAD14609
ID AAD14609 standard; CDNA; 10756 BP.
XX
XX AC AAD14609;
XX
XX DT 11-SEP-2003 (revised)
XX
XX DT 06-AUG-2003 (revised)
XX
XX DT 01-NOV-2001 (first entry)
XX
XX DE Dengue virus (DEN)-2/WN-PP1 chimeric cDNA.
XX
XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX OS Dengue virus; type II.
XX
XX OS West Nile virus.
XX
XX OS Chimeric.
XX
XX FH Key Location/Qualifiers
XX
XX FT CDS 97..10305
XX
XX FT /*tag= a
XX
XX FT /product= "DEN-2/WN-PP1 fusion protein"
XX
XX PN WO200160847-A2.
XX
XX PD 23-AUG-2001.
XX
XX PF 16-FEB-2001; 2001WO-US005142.
XX
XX PR 16-FEB-2000; 2000US-0182829P.
XX
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX P-PSDB; AAE07988.
XX
XX WPI; 2001-497162/54.
XX
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX

PS Example 6; Page 300-316; 470pp; English.

CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/WN-PPI fusion protein related to
CC the invention. This fusion protein contains DEN-2 16681 backbone and the
CC premembrane/membrane protein (ppm) and an envelope protein (E) from West
CC Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-
CC SEP-2003 to standardise OS field)

XX SQ Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10756;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163
|||||

RESULT 24
ADG93313
ID ADG93313 standard; DNA; 15159 BP.
XX AC ADG93313;
XX DT 11-MAR-2004 (first entry)
XX DE DEN2 (Tonga/74) cDNA plasmid P2.
XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
XX KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
XX KW dengue virus; delta30; attenuating mutation; humoral response;
XX KW cellular response; non-structural protein; structural protein;
XX KW dengue virus serotype; gene; ds; plasmid P2.
XX OS Dengue virus type 2.
XX PN WO2003092592-A2.
XX PD 13-NOV-2003.
XX PF 25-APR-2003; 2003WO-US013279.
XX PR 03-MAY-2002; 2002US-0377860P.
XX PR 23-DEC-2002; 2002US-0436500P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX PI Hanley K;
XX DR WPI; 2004-022612/02.
XX DR P-PSDB; ADG93314.
XX PT New tetravalent vaccine containing a common nucleotide deletion in the 3'
XX PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
XX PT of disease in humans caused by dengue virus, or for inducing immune
XX PT response.
XX PS Disclosure; SEQ ID NO 46; 181pp; English.

CC This invention relates to a novel immunogenic composition being
CC tetravalent and containing a common nucleotide deletion in the 3'
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or
CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
CC useful in the prevention of disease in humans caused by dengue virus.
CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
CC unique since they contain a common shared attenuating mutation which
CC eliminates the possibility of generating a virulent wild type virus in a
CC subject to be vaccinated since each component of the vaccine possesses
CC the same delta30 attenuating deletion mutation. The vaccine also is able
CC to induce humoral and cellular responses against all of the (non-
CC structural proteins present in each dengue virus serotype. The present
CC invention is that of the DEN2 cDNA plasmid P2 which is related to the
CC invention.

XX SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 12; Length 15159;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAGAAACCGCG 28
DB 136 AATATGCTGAACCGCGAGAGAAACCGCG 163
|||||

RESULT 25
ADG93317
ID ADG93317 standard; DNA; 2426 BP.
XX AC ADG93317;
XX DT 11-MAR-2004 (first entry)
XX DE DEN1 (Puerto Rico/94) CME chimeric region DNA SeqID50.
XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
XX KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
XX KW dengue virus; delta30; attenuating mutation; humoral response;
XX KW cellular response; non-structural protein; structural protein;
XX KW dengue virus serotype; gene; ds; plasmid P2.
XX OS Dengue virus type 1.
XX PN WO2003092592-A2.
XX PD 13-NOV-2003.
XX PF 25-APR-2003; 2003WO-US013279.
XX PR 03-MAY-2002; 2002US-0377860P.
XX PR 23-DEC-2002; 2002US-0436500P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
XX PI Hanley K;
XX DR WPI; 2004-022612/02.
XX DR P-PSDB; ADG93318.
XX PT New tetravalent vaccine containing a common nucleotide deletion in the 3'
XX PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
XX PT of disease in humans caused by dengue virus, or for inducing immune
XX PT response.
XX PS Disclosure; SEQ ID NO 50; 181pp; English.

CC This invention relates to a novel immunogenic composition being
CC tetravalent and containing a common nucleotide deletion in the 3'
CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
CC useful for the development of compounds with a virucide or

CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
 CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
 CC unique since they contain a common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta30 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC) structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN1 CME chimeric region DNA which is related to
 CC the invention.

XX SQ Sequence 2426 BP; 754 A; 509 C; 632 G; 531 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 2426;

Best Local Similarity 96.4%; Pred. No. 0.066; Mismatches 1; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 |||||
 Db 141 AATATGCTGAACCGGAGAGAAACCGCG 168

RESULT 26

AAQ51476

ID AAQ51476 standard; DNA; 10718 BP.

XX AC AAQ51476;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 16-MAY-1994 (first entry)

XX DE DEN1-S275/90 (ECACC V92042111).

XX KW Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
 XX KW DSS; DEN1 polypeptides; ss.

XX OS Dengue virus type 2.

XX FH Key Location/Qualifiers

FT CDS 81..10271

FT FT /*tag= a

FT FT 81..422

FT FT /*tag= b

FT FT /label= C

FT FT 123..422

FT FT /*tag= c

FT FT /label= C'

FT FT 423..695

FT FT /*tag= d

FT FT /label= Prem

FT FT 696..920

FT FT /*tag= e

FT FT /label= M

FT FT 921..2402

FT FT /*tag= f

FT FT /label= E

FT FT 2403..3464

FT FT /*tag= g

FT FT /label= NS1

FT FT 3465..4112

FT FT /*tag= h

FT FT /label= NS2A

FT FT 4113..4499

FT FT /*tag= i

FT FT /label= NS2B

FT FT 4500..6359

FT FT /*tag= j

FT FT /label= NS3

FT FT 6360..6809

FT FT /*tag= k

FT FT /label= NS4A

FT misc_RNA 6810..7556

FT FT /*tag= l

FT FT /label= NS4B

FT FT 7557..10268

FT FT /*tag= m

FT FT /label= NS5

XX PN WO9322440-A1.

XX PD 11-NOV-1993.

XX PF 28-APR-1993; 93WO-CA000182.

XX PR 29-APR-1992; 92GB-00009243.

XX PA (UYSI-) UNIV SINGAPORE NAT.

XX PI Tan Y, Pu J, Tan B, Yap E, Chan Y;

XX DR WPI; 1993-368799/46.

XX DR P-PSDB; AAR43662.

XX PT New Dengue virus type 1 strain - used to obtain prods. for detection,
 XX diagnosis, vaccines and treatment involving virus.
 XX PS Claim 3; Page 20-34; 55pp; English.
 XX CC DEN1 virus, strain S275/90 was isolated from the serum of a dengue
 XX CC haemorrhagic fever (DHF) patient. RNA was isolated from the virus and
 XX CC used to prepare cDNA encoding DEN1 polypeptides. Dengue virus type 1
 XX CC prods. can be used for detection, diagnosis, vaccines (inactivated form)
 XX CC or treatment of DEN1 infections. The sequences given in AAQ51477-86 are
 XX CC oligonucleotides used to prepare cDNA fragments corresp. to Dengue virus
 XX CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 XX CC on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 2; Length 10718;
 Best Local Similarity 96.4%; Pred. No. 0.08;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28

Db 120 AATATGCTGAACCGGAGAGAAACCGCG 147

RESULT 27

AAAD14603

ID AAD14603 standard; cDNA; 10723 BP.

XX AC AAD14603;

XX DT 11-SEP-2003 (revised)

XX DT 01-NOV-2001 (first entry)

XX DE Dengue virus (DEN)-2/1-VP chimeric cDNA.

XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 XX KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX OS Dengue virus; type I.
 XX OS Dengue virus; type II.
 XX OS Chimeric.

XX FH Key Location/Qualifiers

FT CDS 97..10272

FT FT /*tag= a

FT FT /product= "DEN-2/1-VP fusion protein"

XX FT WO200160847-A2.

XX PD 23-AUG-2001.

```
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07982.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 155-170; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VP fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from wild-type DEN-1 16007 virus. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
Best Local Similarity 96.4%; Pred. No. 0.08;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAAACCGCG 28
DB 136 AATATGCTGAACCGCGCGAGAAACCGCG 163

RESULT 28
AADI4604
ID AADI4604 standard; cDNA; 10723 BP.
XX
XX AAD14604;
XX
XX 11-SEP-2003 (revised)
XX 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/1-VV chimeric cDNA.
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
XX immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type I.
XX Dengue virus; type II.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 97..10272
XX /*tag= a
XX /product= "DEN-2/1-VV fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
```

```
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapratvati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07983.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 179-195; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes dengue virus (DEN)-2/1-VV fusion protein related to the
XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
XX comprising a valine at the non-structural protein (NS3)-250 and the
XX capsid protein (C), premembrane/membrane protein (prM) and an envelope
XX protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus.
XX (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 10723 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
Best Local Similarity 96.4%; Pred. No. 0.08;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGCGAGAAACCGCG 28
DB 136 AATATGCTGAACCGCGCGAGAAACCGCG 163

RESULT 29
AADI4602
ID AADI4602 standard; cDNA; 10735 BP.
XX
XX AAD14602;
XX
XX 01-NOV-2001 (first entry)
XX
XX Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
XX
XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; mutein;
XX avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
XX ss.
XX
XX Dengue virus; type I.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 95..10273
XX /*tag= a
XX /product= "DEN-1 PDK-13 protein variant"
XX
XX mutation replace(1323, T)
XX mutation replace(1541, G)
XX mutation /*tag= C
XX mutation replace(1543, A)
```

```
FT mutation /*tag= d
FT replace(1545, G)
FT /*tag= e
FT replace(1567, A)
FT /*tag= f
FT replace(1608, C)
FT /*tag= g
FT replace(2363, A)
FT /*tag= h
FT replace(2695, T)
FT /*tag= i
FT replace(2782, C)
FT /*tag= j
FT replace(5063, G)
FT /*tag= k
FT replace(6048, A)
FT /*tag= l
FT replace(6806, A)
FT /*tag= m
FT replace(7330, A)
FT /*tag= n
FT replace(9445, C)
FT /*tag= o
XX WO200160847-A2.
XX PN
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 16-FEB-2001; 2001WO-US005142.
XX XX
XX PR 16-FEB-2000; 2000US-0182829P.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX DR WPI; 2001-497162/54.
XX DR P-PSDB; AAE07981.
XX XX
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX XX
XX PS Example 1; Page 130-146; 470pp; English.
XX XX
XX CC The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes attenuated dengue-1 (DEN-1) PPK-13 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region
XX SQ Sequence 10735 BP; 3429 A; 2231 C; 2776 G; 2299 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 4; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0, 08;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
|||||
```

```
Db 134 AATATGCTGAACGCGAGAGAAACCGCG 161
RESULT 30
AAD14601
ID AAD14601 standard; cDNA; 10735 BP.
XX AC AAD14601;
XX DT 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX XX Wild-type, virulent DEN-1 16007 cDNA.
XX XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX OS Dengue virus; type I.
XX FH Key Location/Qualifiers
XX FT CDS 95..10273
XX FT /*tag= a
XX FT /product= "DEN-1 16007 protein"
XX XX
XX PN WO200160847-A2.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 16-FEB-2001; 2001WO-US005142.
XX XX
XX PR 16-FEB-2000; 2000US-0182829P.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX DR WPI; 2001-497162/54.
XX DR P-PSDB; AAE07980.
XX XX
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX XX
XX PS Example 1; Page 106-122; 470pp; English.
XX XX
XX CC The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes wild-type, virulent dengue-1 (DEN-1) 16007 virus protein
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX SQ Sequence 10735 BP; 3432 A; 2232 C; 2774 G; 2297 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 4; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0.08;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
|||||
```


Db 134 AATATGCTGAACGCGGAGAAACCGG 161

RESULT 31

ADN98024

ID ADN98024 standard; DNA; 10735 BP.

AC ADN98024;

XX

XX 29-JUL-2004 (first entry)

DE Dengue Virus isolate WestPac complete genome sequence.

KW ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;

KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.

XX Dengue virus.

XX WO2004040263-A2.

XX 13-MAY-2004.

PF 31-OCT-2003; 2003WO-US034823.

XX

PR 31-OCT-2002; 2002US-0422755P.

PR 06-JUN-2003; 2003US-0476513P.

XX

PA (HEAL-) HEALTH RES INC.

XX

XX Wong SJ, Pei-Yong S;

XX

DR WPI; 2004-400223/37.

DR GENBANK; U88535.

XX

XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein

PT reactive with antibody against WNV and cross-reactive with antibody

PT against a flavivirus, useful in diagnosing flavivirus infection caused by

PT DENV, WNV, JEV or SLEV.

XX

PS Disclosure; Fig 39; 212pp; English.

XX

CC The invention relates to a diagnostic kit comprising at least one

CC isolated and purified polypeptide comprising a West Nile Virus (WNV)

CC envelope (E) protein or its immunogenic fragment having a native

CC conformation or non-denatured structure and that is reactive with

CC antibodies against WNV and cross-reactive with antibodies against a

CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus

CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to

CC the complete nucleotide sequence of the DENV isolate WestPac.

XX

SQ Sequence 10735 BP; 3421 A; 2245 C; 2774 G; 2295 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 10735;

Best Local Similarity 96.4%; Pred. No. 0.08;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAAACCGG 28

|||||

Db 134 AATATGCTGAACGCGGAGAAACCGG 161

RESULT 32

AAC68744

ID AAC68744 standard; DNA; 26 BP.

XX

AC AAC68744;

XX

XX 23-FEB-2001 (first entry)

XX

DE Dengue virus type 2 upper primer.

XX

XX Dengue virus; antiinflammatory; haemostatic; antibacterial; sepsis;

KW immunosuppressive; immunomodulator; cardiac; cytostatic; cachexia;

KW

KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;

KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;

KW chronic myelogenous leukaemia; inflammatory bowel disease; PCR primer;

ss.

XX Dengue virus.

OS

PN WO200064479-A1.

XX

XX 02-NOV-2000.

XX

XX 26-APR-2000; 2000WO-US011700.

XX

XX 27-APR-1999; 99US-00301274.

PR

XX (ANTI-) ANTIBODY SYSTEMS INC.

PA

XX

PI Fredeking TM, Ignatyev GM;

XX

XX WPI; 2000-679646/66.

XX

XX Novel compositions comprising tetracycline or tetracycline-like compounds

PT for the treatment and/or prevention of acute inflammatory responses and

PT diseases, e.g. septic shock and immune complex-induced colitis.

XX

PS Example 2; Page 103; 183pp; English.

XX

CC The present sequence was used in an invention relating to novel

CC compositions and methods containing tetracycline or tetracycline-like

CC compounds for treating and/or preventing acute inflammatory responses and

CC diseases. Such diseases include acute inflammatory conditions associated

CC with viral haemorrhagic diseases (including diseases caused by

CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),

CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune

CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and

CC transplanted bone marrow-induced graft-versus-host disease, septic shock,

CC immune complex-induced colitis, cerebrospinal fluid inflammation,

CC multiple sclerosis, inflammatory responses associated with trauma,

CC systemic inflammatory response syndrome (SIRS), adult respiratory

CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease

CC and Crohn's disease

XX

SQ Sequence 26 BP; 11 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 92.9%; Score 26; DB 3; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGGAGAAACCG 26

|||||

Db 1 AATATGCTGAACGCGGAGAAACCG 26

RESULT 33

AAT75917

ID AAT75917 standard; DNA; 28 BP.

XX

AC AAT75917;

XX

XX 15-SEP-1997 (first entry)

XX

XX

DE DEN-2 cloning/sequencing sense primer, D2-134.

XX

XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;

KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;

KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;

KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;

KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.

XX

OS Synthetic.

XX

XX WO9640933-A1.

PN

PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US009209.
 XX
 PR 07-JUN-1995; 95US-00483292.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYMA-) UNIV MAHIDOL AT SALAYA.
 XX
 XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kinney R, Trent DW;
 XX WPI; 1997-052330/05.
 DR
 XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 XX also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadravalent vaccine for protecting against Dengue virus infection.
 PT
 XX Example; Page 100; 261pp; English.
 PS
 XX The sequences given in AAT75909-T76029 are primers which were used in the
 CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the
 CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises
 CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.
 CC The quadravalent vaccine of the invention comprises an attenuated Dengue
 CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3
 CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are
 CC used to protect against infection by all four serotypes of dengue virus,
 CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal
 CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are
 CC used to produce the recombinant protein products of the DNA constructs
 CC which are used in the vaccines
 XX
 SQ Sequence 28 BP; 11 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

 Query Match 92.9%; Score 26; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AATATGCTGAACCGGAGAGAAACCG 26
 |||||
 DB 3 AATATGCTGAACCGGAGAGAAACCG 28

 RESULT 34
 AAD14610
 ID AAD14610 standard; cDNA; 10699 BP.
 XX
 AC AAD14610;
 XX
 DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 DE Wild-type, virulent DEN-3 16562 cDNA.
 XX
 XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal;
 KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
 KW
 XX Dengue virus; type III.
 OS
 XX Key Location/Qualifiers
 FH CDS 95..10267
 FT /*tag= a
 FT /product= "DEN-3 16562 protein"
 XX
 XX WO200160847-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 16-FEB-2001; 2001WO-US005142.
 XX
 XX 16-FEB-2000; 2000US-0182829P.
 XX
 XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;
 XX WPI; 2001-497162/54.
 DR P-PSDB; AA507989.
 XX
 XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 PT
 XX Example 2; Page 325-341; 470pp; English.
 PS
 XX The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present cDNA
 CC sequence encodes wild-type, virulent dengue-3 (DEN-3) 16562 virus protein
 CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
 CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
 CC contains 5' non-coding region followed by a capsid protein (C) encoding
 CC region, premembrane/membrane protein (prM) encoding region, an envelope
 CC protein (E) encoding region, followed by the region encoding non-
 CC structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
 CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 10699 BP; 3437 A; 2224 C; 2779 G; 2259 T; 0 U; 0 Other;

 Query Match 88.6%; Score 24.8; DB 4; Length 10699;
 Best Local Similarity 92.9%; Pred. No. 0.42;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 |||||
 DB 134 AATATGCTGAACCGCGTGAGAAACCGTG 161

 RESULT 35
 AAD14611
 ID AAD14611 standard; cDNA; 10699 BP.
 XX
 AC AAD14611;
 XX
 DT 01-NOV-2001 (first entry)
 DT
 XX Attenuated, vaccine-strain DEN-3 PGMK-30/FRHL-3 variant cDNA.
 DE
 XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 XX Dengue virus; type III.
 OS
 XX Key Location/Qualifiers
 FH CDS 95..10267
 FT /*tag= a
 FT /product= "DEN-3 PGMK-30/FRHL-3 protein variant"
 FT mutation replace(550, C)
 FT /*tag= b
 FT mutation replace(1813, G)
 FT /*tag= c
 FT mutation replace(1838, A)
 FT /*tag= d
 FT mutation replace(1913, G)
 FT /*tag= e


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XX WO2004072274-A1.
XX 26-AUG-2004.
XX 30-JAN-2004; 2004WO-CN000088.
XX 30-JAN-2003; 2003CN-00115272.
XX 30-JAN-2003; 2003CN-00115273.
XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX (TENG-) TENGGEN BIOMEDICAL CO.
XX (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX Pang X;
XX WPI; 2004-625870/60.
XX Virus-like particle vaccines containing dengue virus recombinant replicon
XX as core for carrier, applicable in preventives or/and remedies for tumors
XX like cervical cancer and viral diseases.
XX Example 2; SEQ ID NO 12; 38pp; Chinese.
XX A dengue virus recombinant replicon has a deletion of the complete coding
XX sequence for preM protein of dengue virus and also includes elements of
XX e.g. the non-coding region in the whole of the 5'-end, the coding region
XX of the front 20 amino acids in the C protein, and the coding region of
XX NS1 protein signal; coding regions of all non-structural proteins. The
XX obtained vaccines are useful in producing preventives or/and remedies for
XX cancer like cervical cancer and viral diseases. Such vaccines can
XX efficiently express antigen in infected cells, which is because dengue
XX virus can infect dendritic cells, and can effectively present antigen to
XX provide immunity effect. Different types of dengue virus can be used to
XX repeatedly produce efficient immune response thereby strengthening the
XX body's immune system against the pathogen that contains such antigen.
XX Human papillomavirus (HPV) vaccines were prepared by using a gene-
XX expressing system using of the full-length dengue virus cDNA clone
XX (pRS/FLD2). The recombinant virus vectors were transfected into baby
XX hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
XX lines. This sequence corresponds to an oligonucleotide used in the
XX recombinant replicon of the invention.
XX Sequence 63 BP; 24 A; 14 C; 14 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 85.7%; Score 24; DB 13; Length 63;
XX Best Local Similarity 100.0%; Pred. No. 0.51;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AATATGCTGAACCGGAGAGAAAC 24
XX 19 AATATGCTGAACCGGAGAGAAAC 42
XX
XX RESULT 38
XX ADR47020
XX ID ADR47020 standard; DNA; 63 BP.
XX AC ADR47020;
XX DT 18-NOV-2004 (first entry)
XX DE HPV-16 oligonucleotide #6 for dengue virus vaccine.
XX SS; cytostatic; virucide; dengue virus; recombinant replicon; deletion;
XX preM protein; C protein; NS1 protein signal; vaccine; cervical cancer;
XX viral disease; antigen; dendritic cell; immune response;
XX human papillomavirus.
XX OS Human papillomavirus type 16.
XX PN WO2004072274-A1.
XX
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PD 26-AUG-2004.
XX 30-JAN-2004; 2004WO-CN000088.
XX 30-JAN-2003; 2003CN-00115272.
XX 30-JAN-2003; 2003CN-00115273.
XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX (TENG-) TENGGEN BIOMEDICAL CO.
XX (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX Pang X;
XX WPI; 2004-625870/60.
XX Virus-like particle vaccines containing dengue virus recombinant replicon
XX as core for carrier, applicable in preventives or/and remedies for tumors
XX like cervical cancer and viral diseases.
XX Example 2; SEQ ID NO 17; 38pp; Chinese.
XX A dengue virus recombinant replicon has a deletion of the complete coding
XX sequence for preM protein of dengue virus and also includes elements of
XX e.g. the non-coding region in the whole of the 5'-end, the coding region
XX of the front 20 amino acids in the C protein, and the coding region of
XX NS1 protein signal; coding regions of all non-structural proteins. The
XX obtained vaccines are useful in producing preventives or/and remedies for
XX cancer like cervical cancer and viral diseases. Such vaccines can
XX efficiently express antigen in infected cells, which is because dengue
XX virus can infect dendritic cells, and can effectively present antigen to
XX provide immunity effect. Different types of dengue virus can be used to
XX repeatedly produce efficient immune response thereby strengthening the
XX body's immune system against the pathogen that contains such antigen.
XX Human papillomavirus (HPV) vaccines were prepared by using a gene-
XX expressing system using of the full-length dengue virus cDNA clone
XX (pRS/FLD2). The recombinant virus vectors were transfected into baby
XX hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
XX lines. This sequence corresponds to an oligonucleotide used in the
XX recombinant replicon of the invention.
XX Sequence 63 BP; 24 A; 14 C; 14 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 85.7%; Score 24; DB 13; Length 63;
XX Best Local Similarity 100.0%; Pred. No. 0.51;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AATATGCTGAACCGGAGAGAAAC 24
XX 19 AATATGCTGAACCGGAGAGAAAC 42
XX
XX Db
XX
XX RESULT 39
XX AAF88836
XX ID AAF88836 standard; DNA; 72 BP.
XX AC AAF88836;
XX DT 09-JAN-2003 (first entry)
XX DE Green fluorescent protein PCR primer #1.
XX KW Replicon; structural region; vaccine; subgenomic replicon; gene therapy;
XX structural protein; C protein; preM protein; E protein; immunisation;
XX GFP; green fluorescent protein; PCR; primer; ss.
XX OS Unidentified.
XX PN WO200272803-A2.
XX PD 19-SEP-2002.
XX PF 21-FEB-2002; 2002WO-US006962.
XX
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09-MAR-2001; 2001US-0274684P.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Pang X, Dayton AI, Zhang M;
WPI; 2002-723344/78.
New subgenomic replicon of dengue virus origin comprising a deletion for the sequence coding for C, PreM and/or E structural proteins, useful as vaccines for immunization against dengue virus infection.
Example 2; Page 38; 66pp; English.
This invention describes a novel subgenomic replicon of dengue virus origin comprising a deletion for the sequence coding for C, PreM and E (DeltaCME), for PreM and E (DeltaME), or for E (DeltaE) structural proteins, and/or which is adapted to receive at least a nucleotide sequence without disrupting its replication capabilities. The products of the invention can be used for constructing (1) a vaccine or a therapeutic comprising the subgenomic replicon and a carrier; (2) a dengue virus-like particle comprising the subgenomic replicon, and structural proteins of the homologous dengue virus, which encapsulates the subgenomic replicon; and (3) methods of immunisation and treatment comprising administering to the individual the subgenomic replicon or the dengue virus like particle cited above. The subgenomic replicons are useful in gene therapy as vaccines for immunisation against dengue virus infection. This sequence represents a PCR primer used with AAF8837 to amplify the green fluorescent protein (GFP) gene cloned into the dengue virus delta-pre-M/E replicon, at the site previously occupied by the pre-M/E genes
Sequence 72 BP; 26 A; 12 C; 24 G; 10 T; 0 U; 0 Other;
Query Match 78.6%; Score 22; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAA 22
DB 28 AATATGCTGAAACGCGAGAA 49
RESULT 40
ADR47008
ID ADR47008 standard; DNA; 96 BP.
XX AC ADR47008;
XX DT 18-NOV-2004 (first entry)
XX DE Dengue virus vaccine oligonucleotide #1.
XX KW ss; cytostatic; virucide; dengue virus; recombinant replicon; deletion; preM protein; C protein; NS1 protein signal; vaccine; cervical cancer;
XX KW viral disease; antigen; dendritic cell; immune response;
XX KW human papillomavirus.
XX OS Unidentified.
XX PN WO2004072274-A1.
XX PD 26-AUG-2004.
XX PF 30-JAN-2004; 2004WO-CN000088.
XX PR 30-JAN-2003; 2003CN-00115272.
XX PR 30-JAN-2003; 2003CN-00115273.
XX PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.
XX PA (TENG-) TENGGEN BIOMEDICAL CO.
XX PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX PI Pang X;
XX WPI; 2004-625870/60.
Virus-like particle vaccines containing dengue virus recombinant replicon as core for carrier, applicable in preventives or/and remedies for tumors like cervical cancer and viral diseases.
Example 1; SEQ ID NO 5; 38pp; Chinese.
A dengue virus recombinant replicon has a deletion of the complete coding sequence for preM protein of dengue virus and also includes elements of e.g. the non-coding region in the whole of the 5'-end, the coding region of the front 20 amino acids in the C protein, and the coding region of the NS1 protein signal; coding regions of all non-structural proteins. The obtained vaccines are useful in producing preventives or/and remedies for cancer like cervical cancer and viral diseases. Such vaccines can efficiently express antigen in infected cells, which is because dengue virus can infect dendritic cells, and can effectively present antigen to provide immunity effect. Different types of dengue virus can be used to repeatedly produce efficient immune response thereby strengthening the body's immune system against the pathogen that contains such antigen. Human papillomavirus (HPV) vaccines were prepared by using a gene-expressing system using of the full-length dengue virus cDNA clone (pRS/FLD2). The recombinant virus vectors were transfected into baby hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell lines. This sequence corresponds to an oligonucleotide used in the recombinant replicon of the invention.
Sequence 96 BP; 28 A; 20 C; 27 G; 21 T; 0 U; 0 Other;
Query Match 75.0%; Score 21; DB 13; Length 96;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGA 21
DB 25 AATATGCTGAAACGCGAGAGA 45
Search completed: July 31, 2005, 13:55:10
Job time : 234 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:00:46 ; Search time 1717.5 Seconds
(without alignments)
620.553 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagtctgaacggagagaaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

- EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	20.6	73.6	776	7	CF996467 AGENCOURT
C 2	19.8	70.7	720	7	CF455745 AGENCOURT
C 3	19.6	70.0	301	6	CB078143 h163h04.g
C 4	19.6	70.0	712	7	CF372439 CSECS052D
C 5	19.6	70.0	722	7	CF512147 Cabud0003
C 6	19.6	70.0	734	7	CF512236 Cabud0003
C 7	19.4	69.3	464	2	BE841207 QV4-SN002
C 8	19	67.9	520	9	CR305770 Medicago
C 9	19	67.9	541	7	CV235337 WS01218.B
C 10	19	67.9	559	9	TA262H01Q
C 11	19	67.9	568	8	AQ945692 Sheared D
C 12	19	67.9	576	9	TA140D12P
C 13	19	67.9	580	2	BE776235 MY-12-P-0
C 14	19	67.9	602	1	AL673619 AL673619
C 15	19	67.9	629	1	AL647632 AL647632
C 16	19	67.9	633	6	CA349616 CA349616
C 17	19	67.9	649	6	CA356841 CA356841
C 18	19	67.9	738	9	AG363192 Mus muscu
C 19	19	67.9	768	9	CC504335 CC504335
C 20	19	67.9	870	9	AG186531 Pan trogl
C 21	19	67.9	988	7	CF995511 AGENCOURT
C 22	18.8	67.1	1687	2	BF128456 601810142
C 23	18.6	66.4	407	7	CF198531 EST0126 T
C 24	18.6	66.4	456	4	BG659286 TGESt2ya2

C	25	18.6	66.4	563	7	CF939381
C	26	18.6	66.4	584	8	AQ657703
C	27	18.6	66.4	593	9	FR0021761
C	28	18.6	66.4	636	7	CO300868
C	29	18.6	66.4	640	7	CN876173
C	30	18.6	66.4	642	1	AI135620
C	31	18.6	66.4	671	7	CN882707
C	32	18.6	66.4	675	7	CN879811
C	33	18.6	66.4	683	7	CN818097
C	34	18.6	66.4	684	8	AQ657387
C	35	18.6	66.4	799	9	CL527496
C	36	18.4	65.7	427	9	CG016439
C	37	18.4	65.7	456	2	AQ724090
C	38	18.4	65.7	496	2	AW599272
C	39	18.4	65.7	582	8	BZ130571
C	40	18.4	65.7	655	6	CB020289
C	41	18.4	65.7	672	8	BH100535
C	42	18.4	65.7	675	6	CA112278
C	43	18.4	65.7	695	8	BH929269
C	44	18.4	65.7	697	8	BH549312
C	45	18.4	65.7	743	7	CK326303
C	46	18.4	65.7	743	7	CV487972
C	47	18.4	65.7	750	2	BEG15972
C	48	18.4	65.7	774	8	BZ154086
C	49	18.4	65.7	777	7	CO936529
C	50	18.4	65.7	780	7	CO933555
C	51	18.4	65.7	786	7	CO920445
C	52	18.4	65.7	788	8	BZ132164
C	53	18.4	65.7	790	2	BF678988
C	54	18.4	65.7	792	4	BI753870
C	55	18.4	65.7	824	2	BF620613
C	56	18.4	65.7	879	7	CN176625
C	57	18.4	65.7	1101	9	CNS00K6J
C	58	18.4	65.7	1126	1	AL697344
C	59	18.4	65.7	1253	2	BF690226
C	60	18.4	65.7	1378	4	BG437449
C	61	18.4	65.7	1631	9	AG444826
C	62	18.2	65.0	109	2	BE763966
C	63	18.2	65.0	145	2	BE763557
C	64	18.2	65.0	149	2	BF922597
C	65	18.2	65.0	158	2	AW897358
C	66	18.2	65.0	159	4	BI042399
C	67	18.2	65.0	159	5	BQ345462
C	68	18.2	65.0	168	2	AW897370
C	69	18.2	65.0	168	2	BE763932
C	70	18.2	65.0	169	2	AW890980
C	71	18.2	65.0	173	5	BQ339990
C	72	18.2	65.0	173	5	BQ339990
C	73	18.2	65.0	188	2	BF919968
C	74	18.2	65.0	192	2	BE763930
C	75	18.2	65.0	203	2	AW890996
C	76	18.2	65.0	211	1	AA364439
C	77	18.2	65.0	213	5	BQ340764
C	78	18.2	65.0	224	2	BF920089
C	79	18.2	65.0	222	2	BE763433
C	80	18.2	65.0	234	2	BF922730
C	81	18.2	65.0	242	2	BE764018
C	82	18.2	65.0	245	4	BI040884
C	83	18.2	65.0	248	5	BQ345780
C	84	18.2	65.0	255	2	BE763994
C	85	18.2	65.0	256	1	AA364917
C	86	18.2	65.0	257	2	BE764040
C	87	18.2	65.0	265	2	BE764021
C	88	18.2	65.0	274	2	BF920147
C	89	18.2	65.0	275	2	BF920150
C	90	18.2	65.0	277	5	BQ345888
C	91	18.2	65.0	285	1	AV125367
C	92	18.2	65.0	285	2	AW890999
C	93	18.2	65.0	286	2	BF928031
C	94	18.2	65.0	286	2	BE702324
C	95	18.2	65.0	287	2	BF928047
C	96	18.2	65.0	287	2	BF928047
C	97	18.2	65.0	295	2	BE763192
C	98	18.2	65.0	296	2	BF924560

CF939381	NCESTqab5
AQ657703	Sheared D
AL014632	F.rubripe
CO300868	EKI79552.
CN876173	O20813AAR
AI135620	GH13441.5
CN882707	O10812AAS
CN879811	O10419AAS
CN818097	O30203ABP
AQ657387	Sheared D
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CG016439	ZUAAG30TH
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BZ130571	CH230-394
CB020289	Px67f07.Y
BH100535	RPCI-24-3
CA112278	SCEPLB104
BH929269	Odi81f08.
BH549312	BOHEP93TR
CK326303	Hd_mx23_0
CV487972	AGENCOURT
BEG15972	601279483
BZ154086	CH230-360
CO936529	AGENCOURT
CO933555	AGENCOURT
CO920445	AGENCOURT
BZ132164	CH230-394
BF678988	602153627
BI753870	603027558
BF620613	HVSMC002
CN176625	AGENCOURT
AL077950	Drosophil
AL697344	Alu697344
BF690226	602186576
BG437449	602490665
AG444826	Mus muscu
BE763966	RC4-NT005
BE763557	QV1-NT004
BF922597	QV4-NT025
AW897358	RC4-NN005
BI042399	RC4-NT016
BQ345462	RC4-NT016
AW897370	RC4-NN005
BE763932	RC4-NT005
AW890980	RC4-NT005
BQ339990	RC5-NN018
BF919968	MR1-NT017
BE763930	RC4-NT005
AW890996	RC4-NT005
AA364439	EST5287
BQ340764	PM3-NN026
BF920089	MR1-NT017
BE763433	RCO-NT003
BF922730	CM2-NT017
BE764018	RC4-NT005
BI040884	QV3-NT027
BQ345780	PMO-NT031
BE763994	RC4-NT005
AA364917	EST75596
BE764040	RC4-NT005
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BF920147	MR1-NT017
BF920150	MR1-NT017
BQ345888	PMO-NT031
AV125367	AV125367
AW890999	RC4-NT005
BF928031	I15-NT022
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BF928047	I15-NT022
BE763192	RC6-NT002
BF924560	I15-NT022

98	18.2	65.0	299	1	AA338845	AA338845	EST43849	171	18.2	65.0	7	CK003909	CK003909	AGENCOURT
C 99	18.2	65.0	302	2	BF922613	BF922613	QV4-NT025	172	18.2	65.0	617	AV724852	AV724852	QV4-NT025
C 100	18.2	65.0	304	2	BF922609	BF922609	QV4-NT025	173	18.2	65.0	623	BQ338598	BQ338598	QV4-NT025
C 101	18.2	65.0	309	2	BF933632	BF933632	IL5-NT022	174	18.2	65.0	629	BM688429	BM688429	UI-E-CQO-
C 102	18.2	65.0	315	2	BF822307	BF822307	CM3-RT001	175	18.2	65.0	629	CK002605	CK002605	AGENCOURT
C 103	18.2	65.0	317	1	AA348826	AA348826	EST55339	176	18.2	65.0	631	BF337960	BF337960	602035794
C 104	18.2	65.0	327	8	B62336	B62336	T21E23TR TA	177	18.2	65.0	633	BM686796	BM686796	UI-E-CQO-
C 105	18.2	65.0	329	8	AQ020647	AQ020647	CIT-HGP-2	178	18.2	65.0	634	BF340047	BF340047	602036986
C 106	18.2	65.0	330	1	AA371949	AA371949	EST83791	179	18.2	65.0	637	BF338164	BF338164	602037966
C 107	18.2	65.0	333	2	AW888882	AW888882	RCO-NT001	180	18.2	65.0	645	BF339643	BF339643	602038923
C 108	18.2	65.0	343	1	AA348026	AA348026	EST54687	181	18.2	65.0	646	BF526151	BF526151	602071053
C 109	18.2	65.0	348	1	AV709566	AV709566	BY068267	182	18.2	65.0	652	BF338165	BF338165	602037967
C 110	18.2	65.0	349	5	BY068267	BY068267	BY068267	183	18.2	65.0	653	BG819424	BG819424	6020781667
C 111	18.2	65.0	351	4	BI041501	BI041501	PMO-NT031	184	18.2	65.0	654	BF346112	BF346112	602018660
C 112	18.2	65.0	353	2	BF922611	BF922611	QV4-NT035	185	18.2	65.0	657	BF018697	BF018697	602018660
C 113	18.2	65.0	355	1	AV420631	AV420631	AV420631	186	18.2	65.0	658	CK001828	CK001828	AGENCOURT
C 114	18.2	65.0	355	1	BF944649	BF944649	PMO-NN117	187	18.2	65.0	664	BF526240	BF526240	602071275
C 115	18.2	65.0	355	5	BQ344497	BQ344497	CM2-NT017	188	18.2	65.0	666	AJ451476	AJ451476	602038252
C 116	18.2	65.0	359	5	BQ345890	BQ345890	PMO-NT031	189	18.2	65.0	670	BF340940	BF340940	602038252
C 117	18.2	65.0	368	2	BF342880	BF342880	602015169	190	18.2	65.0	671	AV728966	AV728966	602038252
C 118	18.2	65.0	376	7	R87436	R87436	YM89a10.r1	191	18.2	65.0	671	BF344051	BF344051	602016861
C 119	18.2	65.0	377	2	BF923985	BF923985	CM2-NT017	192	18.2	65.0	671	CR532392	CR532392	602038252
C 120	18.2	65.0	378	2	BE700099	BE700099	MR0-NN008	193	18.2	65.0	672	BM702209	BM702209	UI-E-CQ1-
C 121	18.2	65.0	378	7	H22054	H22054	YM78d01.r1	194	18.2	65.0	676	BF525473	BF525473	602069562
C 122	18.2	65.0	381	1	AV709591	AV709591	AV709591	195	18.2	65.0	678	BF525884	BF525884	602069844
C 123	18.2	65.0	386	9	AG226463	AG226463	Lotus cor	196	18.2	65.0	681	BF345694	BF345694	602019336
C 124	18.2	65.0	387	1	AA321167	AA321167	EST23621	197	18.2	65.0	692	BM686457	BM686457	UI-E-CQO-
C 125	18.2	65.0	397	4	BF960158	BF960158	CM2-NN024	198	18.2	65.0	694	CK002568	CK002568	AGENCOURT
C 126	18.2	65.0	392	2	BF933729	BF933729	CM2-NT017	199	18.2	65.0	701	BF342433	BF342433	602011937
C 127	18.2	65.0	393	6	CD613941	CD613941	56047276J	200	18.2	65.0	713	BG912875	BG912875	6020807455
C 128	18.2	65.0	395	6	CD613940	CD613940	56047276H	201	18.2	65.0	714	BF340186	BF340186	602036562
C 129	18.2	65.0	400	7	H49669	H49669	Y023C07.r1	202	18.2	65.0	717	BF340035	BF340035	602036974
C 130	18.2	65.0	407	2	BF920871	BF920871	MR2-NT013	203	18.2	65.0	719	BG819478	BG819478	602078177
C 131	18.2	65.0	408	2	BF922617	BF922617	QV4-NT025	204	18.2	65.0	719	CF456135	CF456135	AGENCOURT
C 132	18.2	65.0	408	2	BF933696	BF933696	CM2-NT017	205	18.2	65.0	720	AV726810	AV726810	602070345
C 133	18.2	65.0	411	2	BF920210	BF920210	QV2-NT014	206	18.2	65.0	720	BF526793	BF526793	602070345
C 134	18.2	65.0	413	2	BE936245	BE936245	RC4-NN104	207	18.2	65.0	727	BG818708	BG818708	602779024
C 135	18.2	65.0	420	4	BI041630	BI041630	PMO-NT031	208	18.2	65.0	728	BF526512	BF526512	602070818
C 136	18.2	65.0	431	4	BI041628	BI041628	PMO-NT031	209	18.2	65.0	729	BF526684	BF526684	602070520
C 137	18.2	65.0	431	7	W78082	W78082	EST01649 Su	210	18.2	65.0	729	CF457105	CF457105	AGENCOURT
C 138	18.2	65.0	432	2	BF925437	BF925437	CM2-NT017	211	18.2	65.0	748	BG914306	BG914306	6020812444
C 139	18.2	65.0	444	4	BI035799	BI035799	CM3-NT026	212	18.2	65.0	749	BF345039	BF345039	602014383
C 140	18.2	65.0	452	2	BF919956	BF919956	MR1-NT017	213	18.2	65.0	750	AV727650	AV727650	602036983
C 141	18.2	65.0	466	2	BF922612	BF922612	QV4-NT025	214	18.2	65.0	752	BF340044	BF340044	602036983
C 142	18.2	65.0	470	2	BF922620	BF922620	QV4-NT025	215	18.2	65.0	752	BX622852	BX622852	602072852
C 143	18.2	65.0	477	2	AW680872	AW680872	EST372943	216	18.2	65.0	754	CF457039	CF457039	AGENCOURT
C 144	18.2	65.0	482	2	BF922601	BF922601	QV4-NT025	217	18.2	65.0	755	BF337233	BF337233	602035040
C 145	18.2	65.0	484	2	BF933707	BF933707	CM2-NT017	218	18.2	65.0	757	BF341360	BF341360	602013314
C 146	18.2	65.0	491	7	CF355594	CF355594	V-E-129H1	219	18.2	65.0	757	CF453685	CF453685	AGENCOURT
C 147	18.2	65.0	495	2	BF341915	BF341915	602016436	220	18.2	65.0	761	CF453596	CF453596	AGENCOURT
C 148	18.2	65.0	500	4	BM686644	BM686644	UI-E-CQO-	221	18.2	65.0	762	CF453631	CF453631	AGENCOURT
C 149	18.2	65.0	505	6	CB156658	CB156658	K-BST0215	222	18.2	65.0	762	CF453875	CF453875	AGENCOURT
C 150	18.2	65.0	513	5	BQ345488	BQ345488	MR4-NT014	223	18.2	65.0	763	BF525554	BF525554	602069656
C 151	18.2	65.0	527	5	BF215946	BF215946	BP215946	224	18.2	65.0	764	BF342632	BF342632	602013773
C 152	18.2	65.0	533	2	BF526455	BF526455	602070947	225	18.2	65.0	771	CF457181	CF457181	AGENCOURT
C 153	18.2	65.0	538	2	BE699175	BE699175	QV2-NN005	226	18.2	65.0	780	BF339990	BF339990	602036992
C 154	18.2	65.0	540	8	B2895846	B2895846	Narp3_014	227	18.2	65.0	780	BF341215	BF341215	602038357
C 155	18.2	65.0	546	9	TA176H03Q	TA176H03Q	T. brucei	228	18.2	65.0	783	BF453931	BF453931	AGENCOURT
C 156	18.2	65.0	553	4	BM686618	BM686618	UI-E-CQO-	229	18.2	65.0	784	CF456160	CF456160	AGENCOURT
C 157	18.2	65.0	553	9	CNS03K5M	AL247747	Tetraodon	230	18.2	65.0	786	BF340178	BF340178	602036553
C 158	18.2	65.0	556	2	BF924180	BF924180	MR4-NT014	231	18.2	65.0	787	BF337199	BF337199	602035003
C 159	18.2	65.0	560	4	BI038606	BI038606	MR4-NT014	232	18.2	65.0	787	CF457398	CF457398	AGENCOURT
C 160	18.2	65.0	567	2	BF343376	BF343376	602014675	233	18.2	65.0	789	BX844416	BX844416	602038357
C 161	18.2	65.0	573	8	B2896076	B2896076	Narp5_019	234	18.2	65.0	789	CF456755	CF456755	AGENCOURT
C 162	18.2	65.0	580	2	BF340973	BF340973	602038290	235	18.2	65.0	791	BF340556	BF340556	602037195
C 163	18.2	65.0	581	4	BM686463	BM686463	UI-E-CQO-	236	18.2	65.0	792	BF338225	BF338225	602037837
C 164	18.2	65.0	581	5	BF311881	BF311881	BP311881	237	18.2	65.0	795	BF339025	BF339025	602034813
C 165	18.2	65.0	582	5	BF312342	BF312342	BP312342	238	18.2	65.0	796	CF453929	CF453929	AGENCOURT
C 166	18.2	65.0	583	4	BM707034	BM707034	UI-E-CQO-	239	18.2	65.0	796	CF456318	CF456318	AGENCOURT
C 167	18.2	65.0	583	5	BF209711	BF209711	BP209711	240	18.2	65.0	798	BG912063	BG912063	602080925
C 168	18.2	65.0	593	7	CF454482	CF454482	AGENCOURT	241	18.2	65.0	801	BF339253	BF339253	602038571
C 169	18.2	65.0	600	5	BQ636952	BQ636952	he03f08.y	242	18.2	65.0	806	BF339062	BF339062	602034855
C 170	18.2	65.0	613	2	BF342563	BF342563	602013887	243	18.2	65.0	808	AL567923	AL567923	602034855

244	18.2	65.0	809	2	BF340153	602036521	BF340153	602036521	C 317	18.2	65.0	1097	1	AL565081	AL565081
245	18.2	65.0	815	2	BF525761	602069903	BF525761	602069903	C 318	18.2	65.0	1101	9	CNS05ASH	AL328094 Tetraodon
246	18.2	65.0	821	2	BF344598	602015219	BF344598	602015219	C 319	18.2	65.0	1105	1	AL564810	AL564810
247	18.2	65.0	825	2	BF342626	602013764	BF342626	602013764	C 320	18.2	65.0	1108	7	CF455877	CF455877 AGENCOURT
248	18.2	65.0	826	2	BF526276	602071322	BF526276	602071322	C 321	18.2	65.0	1129	7	BF526995	BF526995 602070275
249	18.2	65.0	827	7	CF455569	AGENCOURT	CF455569	AGENCOURT	C 322	18.2	65.0	1134	2	BF341690	BF341690 602016143
250	18.2	65.0	828	2	BF338209	602037821	BF338209	602037821	C 323	18.2	65.0	1144	2	BF344555	BF344555 602014968
251	18.2	65.0	830	2	BF338156	602037957	BF338156	602037957	C 324	18.2	65.0	1163	2	BF344849	BF344849 602014141
252	18.2	65.0	837	2	BF526348	602070614	BF526348	602070614	C 325	18.2	65.0	1246	5	BQ677481	CR591619 full - leng
253	18.2	65.0	840	1	AL564874	AL564874	AL564874	AL564874	C 326	18.2	65.0	1336	3	CR591619	CR591619 full - leng
254	18.2	65.0	845	2	BF344620	602015242	BF344620	602015242	C 327	18.2	65.0	1603	3	CR685951	CR685951 Tetraodon
255	18.2	65.0	846	2	BF338284	602035508	BF338284	602035508	C 328	18.2	65.0	1706	2	BF341581	BF341581 602013595
256	18.2	65.0	846	4	BG818528	602778752	BG818528	602778752	C 329	18.2	65.0	1896	2	BF341513	BF341513 602013515
257	18.2	65.0	847	2	BF340808	602037696	BF340808	602037696	C 330	18.2	65.0	2116	4	BG852594	BG852594 1024034F0
258	18.2	65.0	852	2	BF343500	602014613	BF343500	602014613	C 331	18.2	65.0	254	1	AV273660	AV273660 6020343F0
259	18.2	65.0	868	2	BF526131	602038162	BF526131	602038162	C 332	18.2	65.0	324	6	BF960356	BF960356 RCS - NN024
260	18.2	65.0	873	2	BF341029	602038162	BF341029	602038162	C 333	18.2	65.0	324	6	CA409632	CA409632 1173 F - P
261	18.2	65.0	874	2	BF343726	602015384	BF343726	602015384	C 334	18.2	65.0	352	1	AA590763	AA590763 vm21a02.r
262	18.2	65.0	875	2	BF525739	602070072	BF525739	602070072	C 335	18.2	65.0	409	9	AA590763	AA590763 F.rubripe
263	18.2	65.0	876	2	BF340541	602037178	BF340541	602037178	C 336	18.2	65.0	432	1	AJ412375	AJ412375
264	18.2	65.0	879	2	BF342630	602013732	BF342630	602013732	C 337	18.2	65.0	549	9	TA535H02P	TA535H02P
265	18.2	65.0	884	7	CF456336	AGENCOURT	CF456336	AGENCOURT	C 338	18.2	65.0	562	9	CL553485	CL553485 OB. Ba000
266	18.2	65.0	885	2	BF340517	602037151	BF340517	602037151	C 339	18.2	65.0	574	5	BU030479	BU030479 QHJ1511.0
267	18.2	65.0	889	2	BF340899	602038208	BF340899	602038208	C 340	18.2	65.0	581	4	BM082773	BM082773 fu25g03.y
268	18.2	65.0	890	2	BF525917	602069879	BF525917	602069879	C 341	18.2	65.0	583	7	CO480568	CO480568 QO164.TB
269	18.2	65.0	892	2	BF341571	602033580	BF341571	602033580	C 342	18.2	65.0	597	9	FR0021765	FR0021765
270	18.2	65.0	895	2	BF338792	602036222	BF338792	602036222	C 343	18.2	65.0	598	4	BM867622	BM867622 mgc8010Xf
271	18.2	65.0	896	2	BF340481	602037107	BF340481	602037107	C 344	18.2	65.0	627	4	BI509660	BI509660 BB170017A
272	18.2	65.0	898	2	BF338009	602035887	BF338009	602035887	C 345	18.2	65.0	636	6	CA969470	CA969470 CLK006822
273	18.2	65.0	899	2	BF340028	602036967	BF340028	602036967	C 346	18.2	65.0	650	6	BY738913	BY738913
274	18.2	65.0	903	2	BF337815	602035614	BF337815	602035614	C 347	18.2	65.0	653	6	CB850104	CB850104 MRA-1865
275	18.2	65.0	904	2	BF343483	602017587	BF343483	602017587	C 348	18.2	65.0	659	5	BQ103758	BQ103758 ESTBB1700
276	18.2	65.0	904	2	BF526612	602070728	BF526612	602070728	C 349	18.2	65.0	664	2	BB635413	BB635413
277	18.2	65.0	907	2	BF341781	602016287	BF341781	602016287	C 350	18.2	65.0	672	2	AW687277	AW687277 NF007H05R
278	18.2	65.0	910	2	BF342730	602013685	BF342730	602013685	C 351	18.2	65.0	675	8	BZ279852	BZ279852 CH230-308
279	18.2	65.0	913	2	BF338041	602035929	BF338041	602035929	C 352	18.2	65.0	709	8	BZ279852	BZ279852 CH230-308
280	18.2	65.0	914	1	AL566947	AL566947	AL566947	AL566947	C 353	18.2	65.0	712	1	AG760845	AG760845 QGVHO24TH
281	18.2	65.0	916	2	BF338141	602037937	BF338141	602037937	C 354	18.2	65.0	734	5	AX879070	AX879070 bx8790053F
282	18.2	65.0	918	2	BF525533	602069631	BF525533	602069631	C 355	18.2	65.0	745	8	AQ854103	AQ854103 nbxb00053F
283	18.2	65.0	918	9	CG771201	TC850.4.G	CG771201	TC850.4.G	C 356	18.2	65.0	752	9	CR132140	CR132140 Forward 8
284	18.2	65.0	920	2	BF339188	602038436	BF339188	602038436	C 357	18.2	65.0	765	9	CG253787	CG253787 OG1CG94TH
285	18.2	65.0	925	2	BF339656	602038936	BF339656	602038936	C 358	18.2	65.0	776	9	CR816616	CR816616 GROAAA1B
286	18.2	65.0	928	2	BF339140	602038442	BF339140	602038442	C 359	18.2	65.0	799	7	CF724220	CF724220 UI-W-G20-
287	18.2	65.0	928	2	BF526123	602017020	BF526123	602017020	C 360	18.2	65.0	839	8	AZ187511	AZ187511 SP. 1009.A
288	18.2	65.0	933	2	BF343464	602017560	BF343464	602017560	C 361	18.2	65.0	883	7	CO936427	CO936427 AGENCOURT
289	18.2	65.0	946	7	CF456212	AGENCOURT	CF456212	AGENCOURT	C 362	18.2	65.0	921	9	CC700322	CC700322 OGJHX87TV
290	18.2	65.0	949	2	BF338031	602035917	BF338031	602035917	C 363	18.2	65.0	948	9	CB589782	CB589782 AGENCOURT
291	18.2	65.0	950	2	BF343081	602015708	BF343081	602015708	C 364	18.2	65.0	959	6	CG054847	CG054847 PUIIKS8TD
292	18.2	65.0	953	2	BF529034	602040004	BF529034	602040004	C 365	18.2	65.0	993	9	CG054847	CG054847 Mus muscu
293	18.2	65.0	954	2	BF526043	602071148	BF526043	602071148	C 366	18.2	65.0	1058	9	AG356625	AG356625 Mus muscu
294	18.2	65.0	955	2	BF525936	602070104	BF525936	602070104	C 367	18.2	65.0	1080	9	CL647416	CL647416 CH213-138
295	18.2	65.0	957	2	BF526560	602070870	BF526560	602070870	C 368	18.2	65.0	1163	9	CL641642	CL641642 CH213-15H
296	18.2	65.0	958	2	BF343797	602015462	BF343797	602015462	C 369	18.2	65.0	1211	3	AK040120	AK040120 Mus muscu
297	18.2	65.0	959	2	BF337322	602034703	BF337322	602034703	C 370	18.2	65.0	1214	9	CL082979	CL082979 ISBI-1D20
298	18.2	65.0	961	2	BF528370	602043707	BF528370	602043707	C 371	17.8	63.6	400	4	BI584713	BI584713 RH23976.5
299	18.2	65.0	964	5	BU485647	603847639	BU485647	603847639	C 372	17.8	63.6	453	4	BI574190	BI574190 RH22922.5
300	18.2	65.0	974	2	BF525632	602069747	BF525632	602069747	C 373	17.8	63.6	590	4	BI587424	BI587424 RH28096.5
301	18.2	65.0	977	2	BF339111	602038411	BF339111	602038411	C 374	17.8	63.6	592	4	BI631268	BI631268 RH60812.5
302	18.2	65.0	986	1	AL565650	AL565650	AL565650	AL565650	C 375	17.8	63.6	593	4	BI593544	BI593544 RH11641.5
303	18.2	65.0	987	8	CC297535	CH261-105	CC297535	CH261-105	C 376	17.8	63.6	598	4	BI594689	BI594689 RH23946.5
304	18.2	65.0	992	2	BF344521	602014929	BF344521	602014929	C 377	17.8	63.6	638	4	BI574629	BI574629 RH22930.5
305	18.2	65.0	1000	7	CF455859	AGENCOURT	CF455859	AGENCOURT	C 378	17.8	63.6	666	4	BI574556	BI574556 RH24493.5
306	18.2	65.0	1007	5	EX406938	EX406938	EX406938	EX406938	C 379	17.8	63.6	666	4	BI605401	BI605401 RH70993.5
307	18.2	65.0	1017	5	EX406938	EX406938	EX406938	EX406938	C 380	17.8	63.6	689	6	CA156073	CA156073 SCEPR2304
308	18.2	65.0	1032	2	BF339993	602036926	BF339993	602036926	C 381	17.8	63.6	694	4	BI586335	BI586335 RH26261.5
309	18.2	65.0	1034	2	BF525573	602069679	BF525573	602069679	C 382	17.8	63.6	694	8	BZ984187	BZ984187 PUGHK70TD
310	18.2	65.0	1042	2	BF526772	602070320	BF526772	602070320	C 383	17.8	63.6	848	7	CB308498	CB308498 SB02046B2
311	18.2	65.0	1065	1	AL532605	AL532605	AL532605	AL532605	C 384	17.8	63.6	852	8	BH658144	BH658144 BOMGT78TR
312	18.2	65.0	1069	2	BF344251	602017313	BF344251	602017313	C 385	17.8	63.6	925	4	BM019356	BM019356 602037296
313	18.2	65.0	1073	5	BM946332	BM946332	BM946332	BM946332	C 386	17.8	63.6	1186	4	BM019356	BM019356 603647513
314	18.2	65.0	1081	2	BF344362	602014740	BF344362	602014740	C 387	17.6	62.9	153	1	AV279194	AV279194 603647513
315	18.2	65.0	1083	2	BF525551	602096562	BF525551	602096562	C 388	17.6	62.9	240	5	BQ698827	BE716189 CM1-H07076
316	18.2	65.0	1084	2	BF345568	602019158	BF345568	602019158	C 389	17.6	62.9	247	5	BQ698827	XXNV064F1

390	17.6	62.9	247	6	CD027812	CD027812 NXNV064F1	c 463	17.6	62.9	741	9	CG420304	CG420304 ZMMBBc003
391	17.6	62.9	290	2	BB086741	BB086741 BB086741	464	17.6	62.9	743	7	W25963	W25963 18a6 Human
c 392	17.6	62.9	318	2	BF824258	BF824258 NCST3a34	465	17.6	62.9	749	7	CK126720	CK126720 AGNCOURT
393	17.6	62.9	325	9	CR491666	CR491666 Medicago	c 466	17.6	62.9	763	9	CG050375	CG050375 PUJAL18TB
394	17.6	62.9	325	9	CG526041	CG526041 OST102148	467	17.6	62.9	772	8	BZ070651	BZ070651 LK29A05
395	17.6	62.9	330	6	BY778929	BY778929 BY778929	468	17.6	62.9	781	7	CN991502	CN991502 68194_125
396	17.6	62.9	331	5	BY782961	BY782961 BY782961	469	17.6	62.9	783	7	CR819063	CR819063 GROAA47B
397	17.6	62.9	333	6	BY103109	BY103109 BY103109	470	17.6	62.9	794	7	CO487831	CO487831 GQ0253b.B
398	17.6	62.9	347	5	BY062936	BY062936 BY062936	471	17.6	62.9	799	9	CR705245	CR705245 OGTAJ51TM
c 399	17.6	62.9	353	7	CR521675	CR521675 CR521675	472	17.6	62.9	803	9	CR302929	CR302929 Medicago
c 400	17.6	62.9	367	5	BY066031	BY066031 BY066031	473	17.6	62.9	811	7	CO486932	CO486932 GQ0224.B7
c 401	17.6	62.9	367	5	CR492050	CR492050 Medicago	474	17.6	62.9	813	9	BX136279	BX136279 Danio rer
c 402	17.6	62.9	397	2	AW290278	AW290278 NXNV017F0	475	17.6	62.9	840	9	CNS01EC9	ANopheles
c 403	17.6	62.9	397	6	CD026924	CD026924 NXNV017F0	c 476	17.6	62.9	863	9	CG705240	CG705240 OGTAJ51TC
c 404	17.6	62.9	410	6	CA906548	CA906548 PCSC16023	477	17.6	62.9	872	7	CO815655	CO815655 AGNCOURT
c 405	17.6	62.9	424	7	CN631929	CN631929 taf45G02.	c 478	17.6	62.9	879	7	CK202451	CK202451 FGAS01097
c 406	17.6	62.9	425	5	BU012463	BU012463 QG31P22.Y	479	17.6	62.9	882	8	AQ576275	AQ576275 nbxb0088L
c 407	17.6	62.9	432	5	BY287560	BY287560 BY287560	480	17.6	62.9	895	9	CG207205	CG207205 OGWBG34TH
c 408	17.6	62.9	436	7	CO104361	CO104361 GR_ED003	481	17.6	62.9	898	9	CG143486	CG143486 PUFUG70TD
c 409	17.6	62.9	436	7	CO130918	GR_ED003	482	17.6	62.9	900	5	BU510337	BU510337 AGNCOURT
c 410	17.6	62.9	442	7	CN967169	CN967169 14666_100	483	17.6	62.9	917	7	CF823497	CF823497 EST700879
c 411	17.6	62.9	449	1	AV817480	AV817480 AV817480	c 484	17.6	62.9	919	6	CD501786	CD501786 CDA52-G05
c 412	17.6	62.9	459	2	BF060459	BF060459 NXCI_115	485	17.6	62.9	923	9	BX957902	BX957902 Forward s
c 413	17.6	62.9	460	1	A1548284	A1548284 UI-R-C3-E	486	17.6	62.9	923	9	CNS06SU1	AL413315 T3 end of
c 414	17.6	62.9	465	6	CD555686	CD555686 B0396C10-	487	17.6	62.9	937	9	CG143486	CG143486 PUFUG70TD
c 415	17.6	62.9	479	9	BX991083	BX991083 Forward s	488	17.6	62.9	942	9	CG189837	CG189837 PUFUG70TD
c 416	17.6	62.9	491	2	BF232342	BF232342 UI-R-C3-E	489	17.6	62.9	954	4	BG343497	BG343497 HVSMEG000
c 417	17.6	62.9	497	1	AJ648532	AJ648532 AJ648532	490	17.6	62.9	960	9	CNS06PEG	CG189837 PUFUG70TD
c 418	17.6	62.9	501	2	BES43085	BES43085 G01069022	c 491	17.6	62.9	964	9	CL129867	CL129867 T3 end of
c 419	17.6	62.9	506	6	CA541825	CA541825 C0611B06-	492	17.6	62.9	978	7	CK272787	CK272787 EST718865
c 420	17.6	62.9	515	7	CO219541	CO219541 WS0107.B2	493	17.6	62.9	1010	9	CNS05F63	CL283550 Tetraodon
c 421	17.6	62.9	519	5	BX254779	BX254779 BX254779	494	17.6	62.9	1011	9	CL283550	CL283550 ZMMBB0062
c 422	17.6	62.9	525	8	AZ650113	AZ650113 1M0520A11	c 495	17.6	62.9	1093	9	CL454953	CL454953 ZMMBB0048
c 423	17.6	62.9	533	4	BG146792	BG146792 mab95H05.	c 496	17.6	62.9	1094	5	BQ215270	BQ215270 AGNCOURT
c 424	17.6	62.9	548	1	AL887606	AL887606 AL887606	c 497	17.6	62.9	1101	9	CNS05588	AL321716 Tetraodon
c 425	17.6	62.9	551	7	CN630418	CN630418 taf35C05.	c 498	17.6	62.9	1106	6	CD518550	CD518550 AGNCOURT
c 426	17.6	62.9	553	1	AL643615	AL643615 AL643615	c 499	17.6	62.9	1112	6	CD505666	CD505666 CDA75-A01
c 427	17.6	62.9	555	2	BB652144	BB652144 BB652144	c 500	17.6	62.9	1114	1	AV712153	AV712153 AV712153
c 428	17.6	62.9	555	8	AQ589567	AQ589567 HS_2107.B							
c 429	17.6	62.9	586	9	CG965190	CG965190 M8EAP67TR							
c 430	17.6	62.9	588	9	CR333379	CR333379 Medicago							
c 431	17.6	62.9	590	9	CL623911	CL623911 OR_BBA001							
c 432	17.6	62.9	601	7	CF142943	CF142943 UI-HF-BP0							
c 433	17.6	62.9	608	9	CR303333	CR303333 Medicago							
c 434	17.6	62.9	609	7	CK442734	CK442734 G00013a.B							
c 435	17.6	62.9	615	7	CN981384	CN981384 49592_126							
c 436	17.6	62.9	618	3	CNS0A861	BX821648 Arabidops							
c 437	17.6	62.9	623	9	CE719084	CE719084 tigr-gss-							
c 438	17.6	62.9	624	2	BB617466	BB617466 BB617466							
c 439	17.6	62.9	626	7	CO118114	CO118114 GR_EB020							
c 440	17.6	62.9	635	7	CN630088	CN630088 taf35C05.							
c 441	17.6	62.9	635	7	CO487501	CO487501 GQ0227.B7							
c 442	17.6	62.9	642	6	CD501785	CD501785 CDA52-G05							
c 443	17.6	62.9	646	2	BB466322	BB466322 BB466322							
c 444	17.6	62.9	648	1	AL851221	AL851221 AL851221							
c 445	17.6	62.9	656	7	CO480716	CO480716 GQ0164.TB							
c 446	17.6	62.9	659	9	CR334095	CR334095 Medicago							
c 447	17.6	62.9	660	9	CR824050	CR824050 ZMMBB016							
c 448	17.6	62.9	661	7	CO232882	CO232882 WS0053.B2							
c 449	17.6	62.9	669	2	BB612601	BB612601 SSH_RIFD1							
c 450	17.6	62.9	669	2	BB065885	BB065885 BB065885							
c 451	17.6	62.9	673	9	CNS02EAY	AL193507 Tetraodon							
c 452	17.6	62.9	675	7	CO118116	CO118116 GR_EB020							
c 453	17.6	62.9	677	2	BB612763	BB612763 BB612763							
c 454	17.6	62.9	677	9	CNS030Y2	AL261764 Tetraodon							
c 455	17.6	62.9	678	9	CR820441	CR820441 SSH_RIFD1							
c 456	17.6	62.9	679	5	BX249091	BX249091 BX249091							
c 457	17.6	62.9	685	2	BE308818	BE308818 601093908							
c 458	17.6	62.9	685	6	CB289521	CB289521 V-B-118A0							
c 459	17.6	62.9	698	7	CO233133	CO233133 WS0057.B2							
c 460	17.6	62.9	698	8	BH983551	BH983551 Ode20g11.							
c 461	17.6	62.9	703	5	BW257462	BW257462 BW257462							
c 462	17.6	62.9	728	7	CO212070	CO212070 WS00923.B							

CF996467
AGNCOURT_16394292 NIH_ZGC_7 Danio rerio cdna clone IMAGE:7037741
5', mRNA sequence.
CF996467
CF996467.1 GI:38517318
EST.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 776)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cdna Library Preparation: Open Biosystems
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14788 row: e column: 03

RESULT 1
CF996467/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

	<p>High quality sequence stop: 734. Location/Qualifiers 1. .776</p> <p>/organism="Danio rerio" /mol_type="mRNA" /db_xref="taxon:7955" /clone="IMAGE:7037741" /tissue_type="whole body" /lab_host="DH10B" /clone_lib="NIH_ZGC_7"</p> <p>/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV; Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH_ZGC_10). Library was constructed by Open Biosystems (Huntsville, AL)"</p> <p>Query Match 73.6%; Score 20.6; DB 7; Length 776; Best Local Similarity 85.2%; Pred. No. 1.4e+02; Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p> <p>QY 2 ATATGCTGAACCGAGAAACCOCG 28 DB 549 ATGTGCTGACCCGAGAGACGCCG 523 </p> <p>RESULT 2 CF455745 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 (bases 1 to 720)</p> <p>NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)</p> <p>Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rml0A07 Bethesda, MD 20892 Email: cgapbs@mail.nih.gov</p> <p>Tissue Procurement: Dr. James R. Lupeki CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>Plate: NDAM581 row: k column: 02 High quality sequence start: 194 High quality sequence stop: 544. Location/Qualifiers 1. .720</p> <p>/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30515857" /tissue_type="Peripheral Nervous system" /lab_host="PH10B (Ti phase-resistant)" /clone_lib="Lupeki anterior_horn" /note="Vector: PCMV-SF0Rf6.I; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned [EcoRV site is destroyed upon cloning]. Average</p> <p>FEATURES source</p>	<p>insert size 2.1 kb. Library was constructed by Invitrogen and donated by J. Lupskei, M.D./Ph.D. (Baylor College of Medicine)."</p> <p>Query Match 70.7%; Score 19.8; DB 7; Length 720; Best Local Similarity 91.3%; Pred. No. 3.3e+02; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p> <p>QY 1 AAATGCTGAACCGAGAGAAA 23 DB 189 AGATGCTGAACCGAGAGAAA 211 </p> <p>RESULT 3 CB078143 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>301 bp mRNA linear EST 24-JAN-2003 hj63h04.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis terminalis cDNA clone hj63h04, mRNA sequence.</p> <p>EST. CB078143 GI:27891580 Hedyotis terminalis Hedyotis terminalis</p> <p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; SpERMatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Rubiaceae; Rubioideae; Spermacoceae; Hedyotis.</p> <p>1 (bases 1 to 301) Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D. Expressed tag sequences from Hedyotis terminalis flower - Stage 2 (NYBG)</p> <p>Unpublished (2003) Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Plate: hj63 row: h column: 04 Seq primer: -21M13UnivRev High quality sequence stop: 301. Location/Qualifiers 1..301</p> <p>/organism="Hedyotis terminalis" /mol_type="mRNA" /db_xref="taxon:219667" /clone="hj63h04" /dev_stage="pre-anthesis; Stage 2" /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)" /note="Organ: flower; Vector: PBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date: Completed 12/18/01. Submitted to CSHL 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TM2562"</p> <p>FEATURES source</p> <p>Query Match 70.0%; Score 19.6; DB 6; Length 301; Best Local Similarity 84.6%; Pred. No. 3.8e+02; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p> <p>QY 3 TATGCTGAACCGAGAGAACCCGG 28 DB 212 TATGCTGAACCGAGAGAACCCGG 237 </p> <p>RESULT 4 CF372439 LOCUS</p> <p>712 bp mRNA linear EST 27-AUG-2003</p>
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DEFINITION CSECS052D08_Flon0012 CabSau Normalised Flower Stage 12 (FLon0012)
Vitis vinifera cDNA clone CSECS052D08 3', mRNA sequence.
ACCESSION CF372439
VERSION CF372439.1 GI:34319685
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 712)
Iocco,P., Hua,C., Davies,C. and Thomas,M.R.
Expressed sequence tags from the grapevine cultivar Cabernet
Sauvignon
Contact: Mark R. Thomas
CSIRO Plant Industry
CSIRO
PO Box 350, Glen Osmond, SA, 5064, Australia
Tel: 61 8 83038600
Fax: 61 8 83038601
Email: Mark.R.Thomas@csiro.au
Seq primer: CCCAGTCACGAGCTGTAAACG (M13 Forward)
POLYA=yes.
FEATURES             source
    1..712
        /organism="Vitis vinifera"
        /mol_type="mRNA"
        /cultivar="Cabernet Sauvignon"
        /db_xref="taxon:29760"
        /clone="CSECS052D08"
        /sex="Hermaphrodite"
        /dev_stage="12 - modified E-L system"
        /clone_lib="CabSau Normalised Flower Stage 12 (FLon0012)"
        /note="Organ: Inflorescence including flowers; Vector:
pZL; Normalised cDNA library from immature inflorescences
at stage 12 of the modified E-L system. Tissue collected
from field grown plants. A description of the modified E-L
system can be found in the paper by B. G. Coombe 'Adoption
of a system for identifying grapevine growth stages'
(1995) Aust. J. Grape and Wine Res. 1: 104-110."
ORIGIN
Query Match          70.0%; Score 19.6; DB 7; Length 712;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCG 26
|||||
Db 374 ATTATGCTGAACCTCGAAGAAACTG 399

RESULT 5
CF512147/c
LOCUS CF512147.1
DEFINITION CF512147 722 bp mRNA linear EST 09-SEP-2003
Cabud0003 IF A10 Vitis vinifera cv. Cabernet sauvignon (Clone 8)
Bud - CABUD Vitis vinifera cDNA clone Cabud0003_IF_A10 5', mRNA
sequence.
ACCESSION CF512147
VERSION CF512147.1 GI:34543915
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 722)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF512147/c
LOCUS CF512147.1
DEFINITION CF512147 734 bp mRNA linear EST 09-SEP-2003
Cabud0003 IR A10 Vitis vinifera cv. Cabernet sauvignon (Clone 8)
Bud - CABUD Vitis vinifera cDNA clone Cabud0003_IR_A10 3', mRNA
sequence.
ACCESSION CF512236
VERSION CF512236.1 GI:34544004
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
FEATURES             source
    1..722
        /organism="Vitis vinifera"
        /mol_type="mRNA"
        /cultivar="Cabernet Sauvignon (Clone 8)"
        /db_xref="taxon:29760"
        /clone="Cabud0003_IF_A10"
        /sex="Hermaphrodite"
        /dev_stage="Pre-bloom (10-11 days before bloom)"
        /lab_host="DH5alpha"
        /clone_lib="Vitis vinifera cv. Cabernet Sauvignon (Clone
8) Bud - CABUD"
        /note="Organ: Bud; Vector: pDNR; Site 1: Sfil; Site 2:
Sfil; CABUD is a cDNA library of Vitis vinifera cv.
'Cabernet Sauvignon' Clone 8 dissected buds. Samples were
collected May 13, 2002 from pre-bloom plants (10-11 days
before bloom), pre-veraison. Sampled vines were located at
the University of California, Davis, Experimental
Vineyard. cDNAs were made by oligo-dT priming and
directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AGCAGCTGTATCAACGCGAGTGCCATTACGCGGG-3' and
5'-ATTCTAGAGCCGAGCGCGACATG-DT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."
ORIGIN
Query Match          70.0%; Score 19.6; DB 7; Length 722;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCG 26
|||||
Db 350 ACTATGCTGAACCTCGAAGAAACTG 325

RESULT 6
CF512236
LOCUS CF512236.1
DEFINITION CF512236 734 bp mRNA linear EST 09-SEP-2003
Cabud0003 IR A10 Vitis vinifera cv. Cabernet sauvignon (Clone 8)
Bud - CABUD Vitis vinifera cDNA clone Cabud0003_IR_A10 3', mRNA
sequence.
ACCESSION CF512236
VERSION CF512236.1 GI:34544004
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 734)
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon (Clone 8)"
/db_xref="taxon:29760"
/clone="Cabud003_IR A10"
/sex="Hermaphrodite"
/dev_stage="pre-bloom (10-11 days before bloom)"
/lab_host="DH5alpha"
/clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD"
/notes="Organ: Bud; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CABUD is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AGCAGTGTATCAAGCGAGAGTGGCCATTACGCCGGG-3' and
5'-ATTCTAGAGCGGAGCGCGGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Query Match 70.0%; Score 19.6; DB 7; Length 734;
Best Local Similarity 84.6%; Pred. No. 4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCG 26
Db 373 ACTATGCTGAACCTCGAAGAACTG 398

RESULT 7
BE841207/c
LOCUS BE841207 464 bp mRNA linear EST 22-SEP-2000
DEFINITION QV4-SN0024-200700-304-a07 SN0024 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE841207
VERSION BE841207.1 GI:10273585
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 464)
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., de Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=QV4-SN0024-200700-304-a07&t3=2000-07-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 248.
Location/Qualifiers

ORIGIN
Query Match 67.9%; Score 19; DB 9; Length 520;
Best Local Similarity 81.5%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCGC 27
Db 241 AACAGGCTGCAACGTCGAAAGAAACCGC 267

RESULT 9
CV235337
LOCUS CV235337 541 bp mRNA linear EST 21-SEP-2004
DEFINITION WS01218.B21 L22 PT-GT-FL-A-3 Populus balsamifera subsp. trichocarpa cDNA clone WS01218_L22_3', mRNA sequence.
ACCESSION CV235337
VERSION CV235337.1 GI:52393807
KEYWORDS EST.

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1. 464
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="SN0024"
/notes="Organ: stomach normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 69.3%; Score 19.4; DB 2; Length 464;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TGCTGAACCGGAGAGAACCC 25
Db 329 TGCTGAACCGGAGAGAACCC 309

RESULT 8
CR305770
LOCUS CR305770 520 bp DNA linear GSS 01-MAR-2004
DEFINITION Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.
ACCESSION CR305770
VERSION CR305770.1 GI:44851914
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 520)
AUTHORS Direct Submission
TITLE Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr
FEATURES
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1..520
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
/notes="Vector: pIndigoBAC ; Site 1: EcoRI ; Site 2: EcoRI ; DeBelle F. and Chalhoub B.-Genoscope sequence ID : mtel-25N13RM1"

ORIGIN
Query Match 67.9%; Score 19; DB 9; Length 520;
Best Local Similarity 81.5%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAACCGC 27
Db 241 AACAGGCTGCAACGTCGAAAGAAACCGC 267

RESULT 9
CV235337
LOCUS CV235337 541 bp mRNA linear EST 21-SEP-2004
DEFINITION WS01218.B21 L22 PT-GT-FL-A-3 Populus balsamifera subsp. trichocarpa cDNA clone WS01218_L22_3', mRNA sequence.
ACCESSION CV235337
VERSION CV235337.1 GI:52393807
KEYWORDS EST.

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QY 1 ATATGCTGAACGCGAGAGAACCGC 27
Db 579 AATATGCAAGAACTGCGAGAGAACTGC 605

RESULT 17
CA356841 649 bp mRNA linear EST 05-NOV-2002
LOCUS 629106 NCCWA lrt Oncorhynchus mykiss cDNA clone lrt100m13_A.G07
DEFINITION 5', mRNA sequence.
ACCESSION CA356841
VERSION CA356841.1 GI:24602028
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 649)
Rexroad,C.E. 3rd, Lee,Y., Keele,J.W., Karamycheva,S., Brown,G.,
Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.
Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGGATAACAATTTTACACAGGA.
FEATURES
source
1..649
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/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="lrt100m13_A.G07"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCWA lrt"
/notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."
ORIGIN
Query Match 67.9%; Score 19; DB 6; Length 649;
Best Local Similarity 81.5%; Pred. No. 7.5e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATATGCTGAACGCGAGAGAACCGC 27
Db 469 AATATGCAAGAACTGCGAGAGAACTGC 495

RESULT 18
AG363192/c 738 bp DNA linear GSS 03-JUN-2004
LOCUS AG363192 Mus musculus molossinus DNA, clone:MSMg01-164N14.TV, genomic survey
DEFINITION sequence.
ACCESSION AG363192
VERSION AG363192.1 GI:47974397
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01

```

```

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 738)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Toskuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
Phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
FEATURES
source
1..738
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-164N14.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match 67.9%; Score 19; DB 9; Length 738;
Best Local Similarity 81.5%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATATGCTGAACGCGAGAGAACCGC 27
Db 690 AATATACCGAAAGCGAGGAAAGCGC 664

RESULT 19
CC504335 768 bp DNA linear GSS 17-JUN-2003
LOCUS CH240_344G2.T7 CHORI-240 Bos taurus genomic clone CH240_344G2,
DEFINITION genomic survey sequence.
ACCESSION CC504335
VERSION CC504335.1 GI:31822628
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 768)
Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schrein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other_GSSs: CH240_344G2.TARBAC13P2
CONTACT: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-8276
Email: rholt@bccsc.ca

```

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering-information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Seq primer: T7

Plate: 344 row: G column: 2

Class: BAC ends.

Location/Qualifiers

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1. .768
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_344G2"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull LI Domino 9915; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
```

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 768;
 Best Local Similarity 81.5%; Pred. No. 7.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
QY 2 ATATGCTGAACGCGAGAGAAACCGCG 28
|||||
DB 86 ATGTACAGAAACGTGAGAGAAACACG 112
|||||
```

RESULT 20
 AG186531/c
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: RP43-060P05.TJ, genomic survey sequence.
 ACCESSION AG186531 GI:16716211
 VERSION AG186531.1
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of Library RPCI-43
 Unpublished
 2 (bases 1 to 870)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (e-mail: chimbases@sc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
 Sequencing: TJ
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1. .870
 /organism="Pan troglodytes"

FEATURES
 source

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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-060P05.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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Query Match 67.9%; Score 19; DB 9; Length 870;
 Best Local Similarity 81.5%; Pred. No. 7.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 2 ATATGCTGAACGCGAGAGAAACCGCG 28
|||||
DB 690 ATATGCGAATCGCGAGAGCAACGCG 664
|||||
```

RESULT 21
 CF995511/c
 LOCUS
 DEFINITION IMAGENCOURT 16028690 NIH_MGC.217 Homo sapiens cDNA clone
 IMAGENCOURT 16028690 5', mRNA sequence.
 ACCESSION CF995511
 VERSION CF995511.1 GI:38512120
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 988)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-rc@mail.nih.gov
 Tissue procurement: James Martin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Plate: NDAM603 row: a column: 15
 High quality sequence stop: 407.

FEATURES source

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1. .988
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524078"
/cisue_type="Pooled Chondrosarcoma Tumor cells"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 217"
/notes="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to RNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5'(AATTCGGCAGG)3' and 5'd
(CCTCGTGGCG)3'. 3' Linker sequence - GCGGCGGTGAGAGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(AATACCTCACTAAGGGA)3'. 5' End: T7 promoter primer 5'd
(TAATACGACTCACTATAGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."
```

ORIGIN

```

Query Match      67.9%; Score 19; DB 7; Length 988;
Best Local Similarity 81.5%; Pred. No. 7.7e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 727 ATTATGCGGAACGAGAGATTAACCGC 701

RESULT 22
LOCUS BF128456
DEFINITION 601810142R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053059 3',
    mRNA sequence.
ACCESSION BF128456
VERSION BF128456.1 GI:10967496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
    Email: cgabbs@email.nih.gov
    Tissue Procurement: ATCC
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLCM891 row: c column: 12
    High quality sequence start: 26
    High quality sequence stop: 165.

FEATURES
    source
    1..1687
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:4053059"
        /tissue_type="leiomyosarcoma cell line"
        /lab_host="PH10B (phage-resistant)"
        /clone_lib="NIH MGC 46"
        /notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
        EcoRI; cDNA made by oligo-dT priming. Directionally cloned
        into EcoRI/XhoI sites using the following 5' adaptor:
        GGACACGAG(G). Size-selected >500bp for average insert size
        1.8kb. Library constructed by Ling Hong in the laboratory
        of Gerald M. Rubin (University of California, Berkeley)
        using ZAP-cDNA synthesis kit (Stratagene) and Superscript
        II RT (Life Technologies). Note: this is a NIH_MGC
        Library."

ORIGIN
Query Match      67.1%; Score 18.8; DB 2; Length 1687;
Best Local Similarity 90.9%; Pred. No. 9.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAACGCGAGAGAAACCGC 28
    ||||| ||||| ||||| ||||| |||||
Db 694 CAGACACGCGAGAGAAACCGC 715

RESULT 23
LOCUS CF198531/c
DEFINITION EST0126 Tamarix androssowii leaf Tamarix androssowii cDNA, mRNA
    sequence.
ACCESSION CF198531
VERSION CF198531.1 GI:33392904

KEYWORDS
SOURCE Tamarix androssowii
ORGANISM Tamarix androssowii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Tamaricaceae; Tamarix.
REFERENCE 1 (bases 1 to 407)
AUTHORS Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
TITLE EST acquired from cDNA library of Tamarix androssowii treated with
    NaHCO3
JOURNAL Unpublished (2003)
COMMENT Contact: Yucheng Wang
    Forestry Source and Environment College
    Northeast Forestry University
    Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
    Tel: 086-451-2190607
    Email: WANGYUCHENG1029@YAHOO.COM.CN.

FEATURES
    source
    1..407
        /organism="Tamarix androssowii"
        /mol_type="mRNA"
        /db_xref="taxon:189785"
        /tissue_type="leaf"
        /clone_lib="Tamarix androssowii leaf"

ORIGIN
Query Match      66.4%; Score 18.6; DB 7; Length 407;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAAC 25
    ||||| ||||| ||||| ||||| |||||
Db 328 AATATGCTGAAGAGAGAGAAAC 304

RESULT 24
LOCUS BG559286/c
DEFINITION TgESTya21d01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplasma gondii
    cDNA clone TgESTya21d01.y1 5' similar to TR:O81505 O81505 F9D12.1
    PROTEIN. ; mRNA sequence.
ACCESSION BG559286
VERSION BG559286.1 GI:13801535
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
REFERENCE 1 (bases 1 to 456)
AUTHORS Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajikwa, J.A., White, M.,
    Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,
    Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
    Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I.,
    Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
    Toxoplasma EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: toxo@watson.wustl.edu
    Contact David Sibley (toxos@borcim.wustl.edu) for further
    information relating to organism, libraries, or clone availability.
    Seq primer: -40RP from Gibco
    High quality sequence stop: 408.

FEATURES
    source
    1..456
        /organism="Toxoplasma gondii"
        /mol_type="mRNA"
        /strain="VEG"
        /db_xref="taxon:5811"

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QY 1 ATATGCTGAACGCGAGAGAAC 25
    ||||| ||||| ||||| |||||
Db 12 AATATCTGAACGCGCAATAAAC 36

RESULT 27
PRO021761
LOCUS      593 bp      DNA      linear      GSS 25-FEB-2004
DEFINITION F.rubripes GSS sequence, clone 067111bdl1, genomic survey sequence.
ACCESSION  AL014632
VERSION     AL014632.1 GI:2681000
KEYWORDS   GSS; genome survey sequence.
SOURCE     Takifugu rubripes (Fugu rubripes)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE  1 Elgar,G., Clark,M.S., Smith,S., Warner,S., Edwards,Y.J.,
            Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and
            Brenner,S.
            Generation and analysis of 25 Mb of genomic DNA from the pufferfish
            Fugu rubripes by sequence scanning
            Genome Res. 9 (10), 960-971 (1999)
            10523524
REFERENCE  2 (bases 1 to 593)
            Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
            Williams,G. and Brenner,S.
            Direct Submission
            Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmrc.ac.uk
            Vector: pBluescript II KS
            V type: Phagemid
            PRIMER: KS
DESC:      One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES   source
            1..593
            /organism="Takifugu rubripes"
            /mol_type="genomic DNA"
            /db_xref="taxon:31033"
            /clone="067111bdl1"
            /clone_lib="cosmid 067111"
ORIGIN
Query Match      66.4%; Score 18.6; DB 9; Length 593;
Best Local Similarity 80.8%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATATGCTGAACGCGAGAGAACG 26
    ||||| ||||| ||||| |||||
Db 46 AANATGCTGAAGAGAGAGAGCG 71

RESULT 28
CO300868/c
LOCUS      636 bp      mRNA      linear      EST 25-JUN-2004
DEFINITION EK179552.5prime Exelixis Flytag CK01 pCDNA-SK+ Drosophila
            melanogaster cDNA clone EK179552 5, mRNA sequence.
ACCESSION  CO300868
VERSION     CO300868.1 GI:49222564
KEYWORDS   EST.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 636)
            Kopczyński,C., Platt,D., Campbell,J., Muzong,C., Laufer,A.,
            Peterson,E. and Swimmer,C.
            Exelixis Flytag EST Project CK01 Library
            Unpublished (2004)
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: EK1795 row: E column: 4
            High quality sequence stop: 467.
FEATURES   Location/Qualifiers
            1..636
            /organism="Drosophila melanogaster"
            /mol_type="mRNA"
            /db_xref="taxon:7227"
            /clone="EK179552"
            /clone_lib="Exelixis Flytag CK01 pCDNA-SK+"
            /note="Organ: mixed stage embryos; imaginal disks, and
            adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
            XhoI; Random primed, normalized library from mixed stage
            embryos, imaginal disks, and adult heads."
ORIGIN
Query Match      66.4%; Score 18.6; DB 7; Length 636;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCG 26
    ||||| ||||| ||||| |||||
Db 205 ATATGCTGAACGCGAGACAG 181

RESULT 29
LOCUS      640 bp      mRNA      linear      EST 04-JUN-2004
DEFINITION 020813AARA00897HT (AARA) Royal Gala partially senescing leaf Malus
            x domestica cDNA clone AARA00897, mRNA sequence.
ACCESSION  CN876173
VERSION     CN876173.1 GI:48262413
KEYWORDS   EST.
SOURCE     Malus x domestica (cultivated apple)
ORGANISM   Malus x domestica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE  1 (bases 1 to 640)
            Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,
            McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
            HortResearch Apple EST Project
            Unpublished (2004)
            Contact: Gleave,A.
            Sequencing Facility
            The Horticulture and Food Research Institute of New Zealand Ltd
            120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
            Tel: 00 64 09 815 4200
            Fax: 00 64 09 815 4201
            Email: est@hortresearch.co.nz.
FEATURES   Location/Qualifiers
            1..640
            /organism="Malus x domestica"
            /mol_type="mRNA"
            /db_xref="taxon:3750"
            /clone="AARA00897"
            /tissue_type="Leaf"
            /dev_stage="partially senescing leaf"
            /clone_lib="(AARA) Royal Gala partially senescing leaf"
            /note="Vector: pBK-CMV; Library sequenced by Genesis
            Research & Development"
ORIGIN
Query Match      66.4%; Score 18.6; DB 7; Length 640;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;

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Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 26
|||||

Db 43 ATATCTTGAACGCGAGAGCAGCTG 67
|||||

RESULT 30

LOCUS

AI135620 642 bp mRNA linear EST 02-DEC-2003
GH13441.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH13441.5 similar to CG9322: FBan0009322
GO:[] located on: 3R 87F12-87F12.; 08/12/2002, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AI135620.1 GI:3628178
EST.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

1 (bases 1 to 642)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMMI Drosophila EST Project
Unpublished (2001)
Other ESTs: GH13441.3prime
Contact: Stapleton, M.
BDGP

TITLE

JOURNAL

COMMENT

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic AB003701: arm:3R [9357746,9566163]
estimated-cyto:87F4-87F14: 04/10/2001
Plate: GH.134 row: D column: 5
High quality sequence stop: 593
POLYA=No.

FEATURES

source

1. .642
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH13441"
/sex="male and female"
/dev_stage="adult"
/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."

ORIGIN

Query Match 66.4%; Score 18.6; DB 1; Length 642;
Best Local Similarity 84.0%; Pred. No. 1.le+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

Db

2 ATATGCTGAACGCGAGAGAAACCG 26
|||||

RESULT 31

LOCUS

CN882707 671 bp mRNA linear EST 04-JUN-2004
010812AASB00315GHT (AASB) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASB003156, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CN882707.1 GI:48268949
EST.
Malus x domestica (cultivated apple)
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

1 (bases 1 to 671)

Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,

McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.

HortResearch Apple EST Project

Unpublished (2004)

Contact: Gleave,A.

Sequencing Facility

The Horticulture and Food Research Institute of New Zealand Ltd

120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200

Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

Location/Qualifiers

1. .671

/organism="Malus x domestica"

/mol_type="mRNA"

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/clone="AASB003156"

/tissue_type="Young fruit"

/dev_stage="10 days after full bloom"

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/note="Vector: pBluescript SK(-); Library sequenced by

Genesis Research & Development"

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Best Local Similarity 84.0%; Pred. No. 1.le+03;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 26
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Db 49 ATATCTTGAACGCGAGAGCAGCTG 73
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RESULT 32

LOCUS

CN879811 675 bp mRNA linear EST 04-JUN-2004
010419AAS004412HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASA004412, mRNA sequence.

CN879811

CN879811.1 GI:48266051

EST.

Malus x domestica (cultivated apple)

Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

1 (bases 1 to 675)

Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B.,

McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.

HortResearch Apple EST Project

Unpublished (2004)

Contact: Gleave,A.

Sequencing Facility

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120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

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Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

Location/Qualifiers

1. .675

/organism="Malus x domestica"

/mol_type="mRNA"

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Genesis Research & Development"

ORIGIN


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FEATURES
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
  Zea mays
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  1 (bases 1 to 427)
    Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
    Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
    Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
    Consortium for Maize Genomics
    Unpublished (2002)
    Other_GSSs: ZUAAG30TV
    Contact: Cathy Whitelaw
    TIGR
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301-838-5943
    Fax: 301-838-0208
    Email: whitelaw@tigr.org
    Seq primer: TR
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ORIGIN
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  ORF_F226; YEAST YEJ4 PROTEIN 1, mRNA sequence.
ACCESSION
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VERSION
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KEYWORDS
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  qb12q03.v1 Mosa EST library PPN Physcomitrella patens cDNA clone
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  ORF_F226; YEAST YEJ4 PROTEIN 1, mRNA sequence.
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  DNA
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  GSS 14-JUL-1999
  HS_5375_A2 H09 SP6E RPCI-11 Human Male BAC Library Homo sapiens
  genomic clone Plate=951 Col=18 Row=O, genomic survey sequence.
  AQT24090.1 GI:5483759
  Homo sapiens (human)
  Homo sapiens
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 456)
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  10449764
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
  or from Resear h Genetics (info@resgen.com). BAC end Web Server:
  http://www.htsc.washington.edu
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      EcoRI MethyIase. Size selected DNA was cloned into the
      pBACe3.6 vector at EcoRI sites"

```


[illegible]

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. Oligo(dT)-SL2 PCR based
 library. cDNA PCR products of size >400 nucleotides containing SL2
 on the 5' end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning
 protocol. Intestine RNA was provided by Dr. Douglas Jasmer of
 Washington State University (djasmer@vetmed.wsu.edu).
 Seq primer: SL1 primer
 High quality sequence stop: 525.

FEATURES
 source

1..655
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 /note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
 Site 2: EcoRI; The library was constructed by Claire
 Murphy and Dr. James McCarter at Washington University,
 St. Louis. Oligo(dT)-SL2 PCR based library. cDNA PCR
 products of size >400 nucleotides containing SL2 on the 5'
 end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the Topo TA
 cloning protocol. Intestine RNA was provided by Dr.
 Douglas Jasmer of Washington State University
 (djasmer@vetmed.wsu.edu)."

ORIGIN

Query Match 65.7%; Score 18.4; DB 6; Length 655;
 Best Local Similarity 78.6%; Pred. No. 1.4e+03;
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 Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Search completed: July 31, 2005, 13:48:06
 Job time : 1740.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 12:23:11 ; Search time 71.5 Seconds
(without alignments) 640.780 Million cell up

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgctgaacgcgagagaaaccgcg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 24055568

Minimum DB seq length: 0

Minimum DB seq length: 9
Maximum DB seq length: 200000000

End of the world

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:★

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12	18.4	65.7	1443	4	US-10-042-991-11	Sequence 11, Appl	
13	18.4	65.7	4512	1	US-08-224-391-52	Sequence 52, Appl	
14	18.4	65.7	4512	1	US-08-484-304-52	Sequence 52, Appl	
c	15	18.4	65.7	12980	3	US-08-811-566-5	Sequence 5, Appli
16	18.4	65.7	12980	3	US-09-034-756-5	Sequence 5, Appli	
17	18.2	65.0	601	4	US-09-949-016-23984	Sequence 5, Appli	
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21	18.2	65.0	3033	4	US-09-949-016-295	Sequence 295, App	
22	18.2	65.0	13871	4	US-09-949-016-12037	Sequence 12037, A	
23	18.2	65.0	13871	4	US-09-949-016-15363	Sequence 15363, A	
c	24	18.2	65.0	143155	4	US-09-949-016-11925	Sequence 11925, A
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c 102	16.2	57.9	701	4	US-09-949-016-120780	Sequence 120780,	c 175	15.8	56.4	601	4	US-09-949-016-92949	Sequence 92949, A
c 103	16.2	57.9	630	3	US-09-328-111-693	Sequence 693, App	c 176	15.8	56.4	601	4	US-09-949-016-92950	Sequence 92950, A
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106	16.2	57.9	7028	4	US-09-949-016-4195	Sequence 4195, Ap	c 179	15.8	56.4	601	4	US-09-949-016-131764	Sequence 131764,
107	16.2	57.9	7042	3	US-09-092-508-1	Sequence 1, Appl	c 180	15.8	56.4	601	4	US-09-949-016-182486	Sequence 182486,
108	16.2	57.9	7042	3	US-09-435-115-1	Sequence 1, Appl	c 181	15.8	56.4	601	4	US-09-949-016-182487	Sequence 182487,
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116	16.2	57.9	7171	4	US-09-949-016-971	Sequence 971, App	c 189	15.8	56.4	601	4	US-09-949-016-206945	Sequence 206945,
c 117	16.2	57.9	27923	4	US-09-949-016-13371	Sequence 13371, A	c 190	15.8	56.4	732	4	US-09-602-787A-435	Sequence 435, App
c 118	16.2	57.9	943510	4	US-09-949-016-15095	Sequence 15095, A	c 191	15.8	56.4	783	3	US-09-134-001C-1622	Sequence 1622, Ap
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c 127	16	57.1	954	4	US-09-949-016-150521	Sequence 150521, A	c 200	15.8	56.4	1472	4	US-08-956-171B-555	Sequence 555, App
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c 130	16	57.1	601	4	US-09-949-016-201141	Sequence 201141, A	c 203	15.8	56.4	1891	4	US-09-270-767-11062	Sequence 11062, A
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c 133	16	57.1	954	4	US-09-830-433A-45	Sequence 45, Appl	c 206	15.8	56.4	3137	4	US-09-710-279-3842	Sequence 3842, Ap
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c 136	16	57.1	1674	4	US-09-134-000C-1536	Sequence 1536, Ap	c 209	15.8	56.4	4806	4	US-09-949-016-3561	Sequence 3561, Ap
c 137	16	57.1	2010	4	US-09-302-540-9547	Sequence 9547, Ap	c 210	15.8	56.4	4860	4	US-09-949-016-296	Sequence 296, App
138	16	57.1	2100	4	US-09-540-236-523	Sequence 523, App	c 211	15.8	56.4	5110	4	US-10-101-464A-963	Sequence 963, App
139	16	57.1	3107	2	US-08-813-940-3	Sequence 3, Appl	c 212	15.8	56.4	5391	4	US-08-811-519-2	Sequence 2, Appl
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141	16	57.1	6219	4	US-09-949-016-1013	Sequence 1013, Ap	c 214	15.8	56.4	5873	1	US-07-928-464-4	Sequence 4, Appl
142	16	57.1	12665	3	US-08-961-527-134	Sequence 134, App	c 215	15.8	56.4	5873	5	PCT-US93-07347-4	Sequence 4, Appl
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145	16	57.1	18355	4	US-08-781-986A-67	Sequence 67, Appl	c 218	15.8	56.4	5890	1	US-07-928-464-6	Sequence 6, Appl
146	16	57.1	19446	3	US-08-961-527-51	Sequence 51, Appl	c 219	15.8	56.4	5890	5	PCT-US93-07347-3	Sequence 3, Appl
147	16	57.1	27630	4	US-09-949-016-12722	Sequence 12722, A	c 220	15.8	56.4	5890	5	PCT-US93-07347-5	Sequence 5, Appl
c 148	16	57.1	81001	3	US-09-750-580-1	Sequence 1, Appl	c 221	15.8	56.4	5890	5	PCT-US93-07347-6	Sequence 6, Appl
c 149	16	57.1	89047	4	US-09-596-002-34	Sequence 34, Appl	c 222	15.8	56.4	6295	1	US-08-003-311B-4	Sequence 4, Appl
c 150	16	57.1	109025	4	US-09-949-016-13609	Sequence 13609, A	c 223	15.8	56.4	6295	1	US-08-261-432-4	Sequence 4, Appl
c 151	16	57.1	109025	4	US-09-949-016-17567	Sequence 17567, A	c 224	15.8	56.4	6312	1	US-08-003-311B-3	Sequence 3, Appl
c 152	16	57.1	128779	4	US-09-497-855A-38	Sequence 38, Appl	c 225	15.8	56.4	6312	1	US-08-003-311B-5	Sequence 5, Appl
c 153	16	57.1	135030	4	US-09-949-016-14896	Sequence 14896, A	c 226	15.8	56.4	6312	1	US-08-003-311B-6	Sequence 6, Appl
c 154	16	57.1	181251	4	US-09-949-016-15970	Sequence 15970, A	c 227	15.8	56.4	6312	1	US-08-003-311B-7	Sequence 7, Appl
c 155	16	57.1	198632	4	US-09-949-016-12781	Sequence 12781, A	c 228	15.8	56.4	6312	1	US-08-261-432-3	Sequence 3, Appl
c 156	16	57.1	198637	4	US-09-949-016-17393	Sequence 17393, A	c 229	15.8	56.4	6312	1	US-08-261-432-5	Sequence 5, Appl
c 157	16	57.1	247781	4	US-09-949-016-17193	Sequence 14193, A	c 230	15.8	56.4	6312	1	US-08-261-432-6	Sequence 6, Appl
c 158	16	57.1	254366	4	US-09-822-871-3	Sequence 3, Appl	c 231	15.8	56.4	6312	1	US-08-261-432-7	Sequence 7, Appl
c 159	16	57.1	786431	4	US-09-751-389-3	Sequence 3, Appl	c 232	15.8	56.4	9335	4	US-09-902-540-940	Sequence 940, App
c 160	16	57.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl	c 233	15.8	56.4	11271	4	US-08-956-171B-11	Sequence 11, Appl
c 161	16	57.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl	c 234	15.8	56.4	11271	4	US-08-781-986A-11	Sequence 11, Appl
c 162	15.8	56.4	190	4	US-09-513-999C-10050	Sequence 10050, A	c 235	15.8	56.4	12368	3	US-08-976-459-20	Sequence 20, Appl
c 163	15.8	56.4	405	4	US-09-710-279-3005	Sequence 3005, Ap	c 236	15.8	56.4	12368	4	US-09-956-004-20	Sequence 20, Appl
c 164	15.8	56.4	405	4	US-09-710-279-3045	Sequence 3045, Ap	c 237	15.8	56.4	15100	4	US-09-949-016-14148	Sequence 14148, A
c 165	15.8	56.4	405	4	US-09-710-279-3303	Sequence 3303, Ap	c 238	15.8	56.4	28129	4	US-09-949-016-17168	Sequence 17168, A
c 166	15.8	56.4	423	4	US-09-270-767-7033	Sequence 7033, Ap	c 239	15.8	56.4	28129	4	US-09-949-016-17169	Sequence 17169, A
c 167	15.8	56.4	423	4	US-09-270-767-22315	Sequence 22315, A	c 240	15.8	56.4	28120	4	US-09-949-016-13356	Sequence 13356, A
c 168	15.8	56.4	520	4	US-09-621-976-811	Sequence 811, App	c 241	15.8	56.4	47110	4	US-09-949-016-17609	Sequence 17609, A
c 169	15.8	56.4	573	4	US-09-270-767-1326	Sequence 126, App	c 242	15.8	56.4	48536	4	US-09-949-016-11867	Sequence 11867, A
c 170	15.8	56.4	573	4	US-09-270-767-15408	Sequence 15408, A	c 243	15.8	56.4	48536	4	US-09-949-016-17167	Sequence 17167, A
c 171	15.8	56.4	601	4	US-09-949-016-20277	Sequence 20277, A	c 244	15.8	56.4	66219	4	US-09-949-016-12038	Sequence 12038, A
c 172	15.8	56.4	601	4	US-09-949-016-24007	Sequence 24007, A	c 245	15.8	56.4	66227	4	US-09-949-016-15303	Sequence 15303, A
c 173	15.8	56.4	601	4	US-09-949-016-41972	Sequence 41972, A	c 246	15.8	56.4	84171	4	US-09-949-016-16356	Sequence 16356, A

247	15.8	56.4	84571	4	US-09-949-016-17420	Sequence 17420, A	C 320	15.6	55.7	1830121	4	US-09-557-884-1	Sequence 1, Appli
248	15.8	56.4	87563	3	US-09-453-702B-57	Sequence 57, Appl	C 321	15.6	55.7	1830121	4	US-09-643-990A-1	Sequence 1, Appli
249	15.8	56.4	113283	4	US-09-949-016-16976	Sequence 16976, A	C 322	15.4	55.0	98	4	US-09-513-999C-27844	Sequence 27844, A
250	15.8	56.4	113283	4	US-09-949-016-16977	Sequence 16977, A	C 323	15.4	55.0	126	4	US-09-513-999C-32406	Sequence 32406, A
251	15.8	56.4	116652	4	US-09-949-016-13413	Sequence 13413, A	C 324	15.4	55.0	166	4	US-09-513-999C-27086	Sequence 27086, A
252	15.8	56.4	119649	4	US-09-949-016-12537	Sequence 12537, A	C 325	15.4	55.0	265	4	US-09-270-767-28701	Sequence 28701, A
253	15.8	56.4	135476	4	US-09-949-016-12611	Sequence 12611, A	C 326	15.4	55.0	273	4	US-09-248-796A-10268	Sequence 10268, A
254	15.8	56.4	135476	4	US-09-949-016-14413	Sequence 14413, A	C 327	15.4	55.0	341	3	US-08-123-934A-11	Sequence 11, Appl
255	15.8	56.4	136058	4	US-09-949-016-12865	Sequence 12865, A	C 328	15.4	55.0	341	4	US-09-874-628-11	Sequence 11, Appl
256	15.8	56.4	136480	4	US-09-949-016-17064	Sequence 17064, A	C 329	15.4	55.0	341	5	PCT-US94-10080-11	Sequence 11, Appl
257	15.8	56.4	147321	4	US-09-949-016-15450	Sequence 15450, A	C 330	15.4	55.0	344	4	US-09-513-999C-21564	Sequence 21564, A
258	15.8	56.4	150409	4	US-09-949-016-12290	Sequence 12290, A	C 331	15.4	55.0	351	4	US-09-640-211A-438	Sequence 438, App
259	15.8	56.4	150409	4	US-09-949-016-12938	Sequence 12938, A	C 332	15.4	55.0	360	4	US-09-489-039A-3102	Sequence 3102, Ap
260	15.8	56.4	640681	4	US-09-790-988-1	Sequence 1, Appli	C 333	15.4	55.0	390	4	US-09-270-767-30955	Sequence 30955, A
261	15.6	55.7	315	4	US-09-943-681A-1354	Sequence 1354, Ap	C 334	15.4	55.0	439	4	US-09-270-767-12782	Sequence 12782, A
262	15.6	55.7	601	4	US-09-949-016-66060	Sequence 66060, A	C 335	15.4	55.0	462	4	US-09-573-080A-249	Sequence 249, App
263	15.6	55.7	601	4	US-09-949-016-79456	Sequence 79456, A	C 336	15.4	55.0	468	4	US-09-328-352-935	Sequence 935, App
264	15.6	55.7	601	4	US-09-949-016-113199	Sequence 113199, A	C 337	15.4	55.0	488	4	US-09-621-976-12091	Sequence 12091, A
265	15.6	55.7	601	4	US-09-949-016-151417	Sequence 151417, A	C 338	15.4	55.0	601	4	US-09-949-016-21814	Sequence 21814, A
266	15.6	55.7	601	4	US-09-949-016-151418	Sequence 151418, A	C 339	15.4	55.0	601	4	US-09-949-016-23218	Sequence 23218, A
267	15.6	55.7	601	4	US-09-949-016-156788	Sequence 156788, A	C 340	15.4	55.0	601	4	US-09-949-016-23219	Sequence 23219, A
268	15.6	55.7	601	4	US-09-949-016-190408	Sequence 190408, A	C 341	15.4	55.0	601	4	US-09-949-016-39838	Sequence 39838, A
269	15.6	55.7	610	4	US-09-573-080A-245	Sequence 245, App	C 342	15.4	55.0	601	4	US-09-949-016-54269	Sequence 54269, A
270	15.6	55.7	750	4	US-09-489-039A-2242	Sequence 2242, Ap	C 343	15.4	55.0	601	4	US-09-949-016-54333	Sequence 54333, A
271	15.6	55.7	782	4	US-09-302-540-7646	Sequence 7646, Ap	C 344	15.4	55.0	601	4	US-09-949-016-83720	Sequence 83720, A
272	15.6	55.7	787	2	US-08-777-321A-2	Sequence 2, Appli	C 345	15.4	55.0	601	4	US-09-949-016-88808	Sequence 88808, A
273	15.6	55.7	787	4	US-09-016-434-254	Sequence 254, App	C 346	15.4	55.0	601	4	US-09-949-016-88809	Sequence 88809, A
274	15.6	55.7	1023	4	US-09-940-244-401	Sequence 401, App	C 347	15.4	55.0	601	4	US-09-949-016-129186	Sequence 129186, A
275	15.6	55.7	1143	4	US-09-543-681A-1740	Sequence 1740, Ap	C 348	15.4	55.0	601	4	US-09-949-016-129187	Sequence 129187, A
276	15.6	55.7	1392	4	US-09-489-039A-2303	Sequence 2303, Ap	C 349	15.4	55.0	601	4	US-09-949-016-130377	Sequence 130377, A
277	15.6	55.7	1502	4	US-09-949-016-963	Sequence 963, App	C 350	15.4	55.0	601	4	US-09-949-016-130378	Sequence 130378, A
278	15.6	55.7	2059	4	US-09-949-016-2006	Sequence 2006, App	C 351	15.4	55.0	601	4	US-09-949-016-131765	Sequence 131765, A
279	15.6	55.7	2478	3	US-09-215-694-31	Sequence 31, Appl	C 352	15.4	55.0	601	4	US-09-949-016-141756	Sequence 141756, A
280	15.6	55.7	2823	4	US-09-328-352-4039	Sequence 4039, Ap	C 353	15.4	55.0	601	4	US-09-949-016-160861	Sequence 160861, A
281	15.6	55.7	3901	1	US-08-326-297-1	Sequence 1, Appli	C 354	15.4	55.0	601	4	US-09-949-016-200651	Sequence 200651, A
282	15.6	55.7	3901	3	US-08-617-454-1	Sequence 1, Appli	C 355	15.4	55.0	601	4	US-09-949-016-200797	Sequence 200797, A
283	15.6	55.7	3901	5	PCT-US94-01144-1	Sequence 1, Appli	C 356	15.4	55.0	714	1	US-07-789-738-3	Sequence 3, Appli
284	15.6	55.7	5032	4	US-09-366-921-14	Sequence 14, Appl	C 357	15.4	55.0	749	4	US-09-602-787A-377	Sequence 377, App
285	15.6	55.7	5822	3	US-08-899-595-4	Sequence 4, Appli	C 358	15.4	55.0	773	1	US-07-789-738-5	Sequence 5, Appli
286	15.6	55.7	5822	3	US-08-899-595-5	Sequence 5, Appli	C 359	15.4	55.0	885	3	US-09-187-050-11	Sequence 11, Appl
287	15.6	55.7	6594	4	US-09-902-540-752	Sequence 752, App	C 360	15.4	55.0	900	4	US-09-949-016-3102	Sequence 3102, Ap
288	15.6	55.7	21116	4	US-09-949-016-13748	Sequence 13748, A	C 361	15.4	55.0	930	3	US-09-280-116-188	Sequence 188, App
289	15.6	55.7	26684	4	US-09-949-016-15109	Sequence 15109, A	C 362	15.4	55.0	936	4	US-09-252-991A-14805	Sequence 14805, A
290	15.6	55.7	26684	4	US-09-949-016-15110	Sequence 15110, A	C 363	15.4	55.0	1059	4	US-09-248-796A-1578	Sequence 1578, A
291	15.6	55.7	26684	4	US-09-949-016-17409	Sequence 17409, A	C 364	15.4	55.0	1102	4	US-09-270-767-11858	Sequence 11858, A
292	15.6	55.7	26684	4	US-09-949-016-17410	Sequence 17410, A	C 365	15.4	55.0	1147	4	US-09-721-908-1	Sequence 1, Appli
293	15.6	55.7	31096	4	US-08-956-171B-59	Sequence 59, Appl	C 366	15.4	55.0	1147	4	US-09-721-341-1	Sequence 1, Appli
294	15.6	55.7	31096	4	US-08-781-986A-59	Sequence 59, Appl	C 367	15.4	55.0	1147	4	US-09-721-341-3	Sequence 3, Appli
295	15.6	55.7	31328	3	US-09-215-694-19	Sequence 19, Appl	C 368	15.4	55.0	1147	4	US-09-721-495B-1	Sequence 1, Appli
296	15.6	55.7	62636	4	US-09-949-016-15464	Sequence 15464, A	C 369	15.4	55.0	1161	4	US-09-252-991A-15064	Sequence 3, Appli
297	15.6	55.7	62636	4	US-09-949-016-15465	Sequence 15465, A	C 370	15.4	55.0	1161	4	US-09-252-991A-15064	Sequence 15064, A
298	15.6	55.7	66627	4	US-09-949-016-12630	Sequence 12630, A	C 371	15.4	55.0	1179	3	US-09-187-050-13	Sequence 13, Appl
299	15.6	55.7	66627	4	US-09-949-016-16112	Sequence 16112, A	C 372	15.4	55.0	1179	3	US-09-187-050-15	Sequence 15, Appl
300	15.6	55.7	87562	4	US-09-949-016-13685	Sequence 13685, A	C 373	15.4	55.0	1179	3	US-09-187-050-17	Sequence 17, Appl
301	15.6	55.7	112623	4	US-09-949-016-14374	Sequence 14374, A	C 374	15.4	55.0	1179	3	US-09-187-050-19	Sequence 19, Appl
302	15.6	55.7	141454	4	US-09-949-016-12055	Sequence 12055, A	C 375	15.4	55.0	1179	3	US-09-187-050-21	Sequence 21, Appl
303	15.6	55.7	141454	4	US-09-949-016-17190	Sequence 17190, A	C 376	15.4	55.0	1179	3	US-09-187-050-23	Sequence 23, Appl
304	15.6	55.7	152655	4	US-09-949-016-16246	Sequence 16246, A	C 377	15.4	55.0	1179	3	US-09-187-050-25	Sequence 25, Appl
305	15.6	55.7	152655	4	US-09-497-855A-40	Sequence 40, Appl	C 378	15.4	55.0	1365	4	US-09-489-039A-5747	Sequence 5747, Ap
306	15.6	55.7	161652	4	US-09-949-016-15999	Sequence 15999, A	C 379	15.4	55.0	1467	4	US-09-489-039A-6192	Sequence 6192, Ap
307	15.6	55.7	169334	4	US-09-949-016-15999	Sequence 15999, A	C 380	15.4	55.0	1517	4	US-09-801-874-1	Sequence 1, Appli
308	15.6	55.7	205044	4	US-09-949-016-15851	Sequence 15851, A	C 381	15.4	55.0	1549	4	US-09-910-695-7	Sequence 7, Appli
309	15.6	55.7	205044	4	US-09-949-016-15852	Sequence 15852, A	C 382	15.4	55.0	1564	4	US-09-270-767-14725	Sequence 17, Appl
310	15.6	55.7	205044	4	US-09-949-016-15853	Sequence 15853, A	C 383	15.4	55.0	1660	2	US-08-966-316-17	Sequence 17, Appl
311	15.6	55.7	223471	4	US-09-949-016-12387	Sequence 12387, A	C 384	15.4	55.0	1660	4	US-09-489-039A-4920	Sequence 4920, Ap
312	15.6	55.7	223471	4	US-09-949-016-12724	Sequence 12724, A	C 385	15.4	55.0	1722	4	US-09-949-016-4171	Sequence 4171, Ap
313	15.6	55.7	223471	4	US-09-949-016-12725	Sequence 12725, A	C 386	15.4	55.0	1743	4	US-09-949-016-4171	Sequence 4171, Ap
314	15.6	55.7	285986	4	US-09-949-016-12887	Sequence 12887, A	C 387	15.4	55.0	1830	4	US-09-107-532A-1456	Sequence 1456, Ap
315	15.6	55.7	288031	4	US-09-949-016-14864	Sequence 14864, A	C 388	15.4	55.0	1836	4	US-09-328-352-1536	Sequence 1536, Ap
316	15.6	55.7	346112	4	US-09-949-016-13165	Sequence 13165, A	C 389	15.4	55.0	1889	3	US-09-187-050-1	Sequence 1, Appli
317	15.6	55.7	784019	4	US-09-949-016-14033	Sequence 14033, A	C 390	15.4	55.0	2363	4	US-09-949-016-2159	Sequence 2159, Ap
318	15.6	55.7	828152	4	US-09-949-016-12777	Sequence 12777, A	C 391	15.4	55.0	2505	3	US-09-614-221A-73	Sequence 73, Appl
319	15.6	55.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli	C 392	15.4	55.0	2625	3	US-09-453-702B-210	Sequence 210, App
	15.6	55.7	1230230	4	US-09-438-185A-1	Sequence 1, Appli		15.4	55.0	2646	4	US-09-799-451-819	Sequence 819, App

C 393 15.4 55.0 2669 4 US-09-799-451-545 Sequence 545, App
394 15.4 55.0 2691 4 US-09-489-039A-3091 Sequence 3091, App
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396 15.4 55.0 2891 4 US-09-949-016-1115 Sequence 1115, Ap
397 15.4 55.0 2891 4 US-09-949-016-4503 Sequence 4503, Ap
398 15.4 55.0 3100 4 US-09-270-767-12855 Sequence 12855, A
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C 407 15.4 55.0 5247 4 US-09-949-016-14844 Sequence 14844, A
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C 413 15.4 55.0 6513 1 US-08-724-095-7 Sequence 7, Appli
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C 425 15.4 55.0 8948 4 US-09-476-496A-119 Sequence 119, App
C 426 15.4 55.0 8948 4 US-09-630-940B-119 Sequence 119, App
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C 444 15.4 55.0 87611 4 US-09-949-016-16139 Sequence 16139, A
C 445 15.4 55.0 87629 4 US-09-949-016-15262 Sequence 15262, A
C 446 15.4 55.0 87629 4 US-09-949-016-15263 Sequence 15263, A
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C 448 15.4 55.0 87629 4 US-09-949-016-15265 Sequence 15265, A
C 449 15.4 55.0 87648 4 US-09-949-016-13655 Sequence 13655, A
C 450 15.4 55.0 89561 4 US-09-949-016-12768 Sequence 12768, A
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C 454 15.4 55.0 101558 4 US-09-949-016-12243 Sequence 12243, A
C 455 15.4 55.0 104520 4 US-09-949-016-13303 Sequence 13303, A
C 456 15.4 55.0 126029 4 US-09-949-016-14731 Sequence 14731, A
C 457 15.4 55.0 142504 4 US-09-949-016-13693 Sequence 13693, A
C 458 15.4 55.0 142506 4 US-09-949-016-12474 Sequence 12474, A
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C 465 15.4 55.0 363033 4 US-09-949-016-15754 Sequence 15754, A

C 466 15.4 55.0 455726 4 US-09-949-016-14157 Sequence 14157, A
C 467 15.4 55.0 580073 4 US-08-545-528B-1 Sequence 1, Appli
C 468 15.4 55.0 786431 4 US-09-751-389-3 Sequence 3, Appli
C 469 15.4 55.0 4403765 3 US-09-103-840A-2 Sequence 2, Appli
C 470 15.4 55.0 4411529 3 US-09-103-840A-1 Sequence 1, Appli
C 471 15.2 54.3 26 4 US-09-940-244-332 Sequence 332, App
C 472 15.2 54.3 231 4 US-09-621-976-14380 Sequence 14380, A
C 473 15.2 54.3 270 3 US-09-134-001C-163 Sequence 163, App
C 474 15.2 54.3 279 4 US-09-513-999C-34355 Sequence 34355, A
C 475 15.2 54.3 348 4 US-09-621-976-16644 Sequence 16644, A
C 476 15.2 54.3 353 4 US-09-621-976-19280 Sequence 19280, A
C 477 15.2 54.3 359 4 US-09-621-976-16649 Sequence 16649, A
C 478 15.2 54.3 384 4 US-09-134-000C-1165 Sequence 1165, Ap
C 479 15.2 54.3 393 4 US-09-489-039A-5316 Sequence 5316, Ap
C 480 15.2 54.3 451 4 US-09-971-806-4 Sequence 4, Appli
C 481 15.2 54.3 462 4 US-09-621-976-17211 Sequence 17211, A
C 482 15.2 54.3 468 4 US-09-506-286B-54 Sequence 54, Appl
C 483 15.2 54.3 468 4 US-10-065-133A-54 Sequence 54, Appl
C 484 15.2 54.3 509 4 US-09-809-665A-53 Sequence 53, Appl
C 485 15.2 54.3 581 3 US-09-221-017B-607 Sequence 607, App
C 486 15.2 54.3 601 4 US-09-949-016-20374 Sequence 20374, A
C 487 15.2 54.3 601 4 US-09-949-016-45509 Sequence 45509, A
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C 492 15.2 54.3 601 4 US-09-949-016-93760 Sequence 93760, A
C 493 15.2 54.3 601 4 US-09-949-016-112388 Sequence 112388, A
C 494 15.2 54.3 601 4 US-09-949-016-112389 Sequence 112389, A
C 495 15.2 54.3 601 4 US-09-949-016-142433 Sequence 142433, A
C 496 15.2 54.3 601 4 US-09-949-016-165297 Sequence 165297, A
C 497 15.2 54.3 601 4 US-09-949-016-202797 Sequence 202797, A
C 498 15.2 54.3 672 4 US-09-252-991A-1284 Sequence 1284, Ap
C 499 15.2 54.3 716 4 US-09-270-767-3457 Sequence 3457, Ap
500 15.2 54.3 716 4 US-09-270-767-18739 Sequence 18739, A

ALIGNMENTS

RESULT 1
US-08-869-423-1
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochel, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Kalish, Daniel
REGISTRATION NUMBER: 33,599
REFERENCE/DOCKET NUMBER: NC 77,654
TELEPHONE: (301) 295-5642
TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: New Guinea C
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Prem and Envelope
MAP POSITION: 330-2446
UNITS: bp
PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
AUTHORS: Woo, W S
AUTHORS: Biedrzycka, A
AUTHORS: Wright, P J
TITLE: Partial nucleotide sequence and deduced amino
TITLE: acid sequence of the structural proteins of dengue
TITLE: virus type 2, New Guinea C and PUO-218 strains
JOURNAL: J. Gen. Virol.
VOLUME: 69
PAGES: 1391-1398
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Irie, K
AUTHORS: Mohan, P M
AUTHORS: Saeguri, Y
AUTHORS: Putnak, R
AUTHORS: Padmanabhan, R
TITLE: Sequence Analysis of Cloned dengue virus type
Patent No. 6455509
TITLE: 2 genome (New Guinea-C strain)
JOURNAL: Gene
VOLUME: 75
ISSUE: 2
PAGES: 197-211
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: Yaegashi, T
AUTHORS: Vakharia, V N
AUTHORS: Page, K
AUTHORS: Saeguri, Y
AUTHORS: Feighny, R
AUTHORS: Padmanabhan, R
JOURNAL: Gene
VOLUME: 46
ISSUE: 2-3
PAGES: 257-267
DATE: 1986
US-08-869-423-1

Query Match 100.0%; Score 28; DB 3; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 60 AATATGCTGAACCGGAGAGAAACCGCG 87
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RESULT 2

US-08-937-195-1
Sequence 1, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PRI59/S1
FEATURE:
NAME/KEY: misc feature
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PRI59 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= (1))
FEATURE:
NAME/KEY: misc feature
LOCATION: 1218
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc feature
LOCATION: 1260
OTHER INFORMATION: /note= "T is replaced by G for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc feature
LOCATION: 1762
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc feature
LOCATION: 1929


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; OTHER INFORMATION: /note= "C is replaced by T for
; OTHER INFORMATION: Wild-Type sequence"
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; NAME/KEY: misc_feature
; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
;
US-08-937-195-1
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAACCGG 28
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Db 40 AATATGCTGAACGCGAGAGAACCGG 67

RESULT 3
US-08-937-195-2
; Sequence 2, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937.195
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2(DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159/S1"
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159/S1"
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159/S1"
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159/S1"
; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= (11)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
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RESULT 5
US-08-915-152-2
; Sequence 2, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
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; OTHER INFORMATION: strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159

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; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
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; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; US-08-915-152-2
;
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 6
US-09-376-463-2
; Sequence 2, Application US/09376463
; Patent No. 6749857
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; FILE REFERENCE: 24733-20005.20
; CURRENT APPLICATION NUMBER: US/09/376,463
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381

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; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-09-376-463-2
Query Match 100.0%; Score 28; DB 4; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 7
PCT-US96-07627-1
; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION.
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
; LOCATION: 1260
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762
; OTHER INFORMATION: /note= "G is replaced by A for
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; NAME/KEY: misc_feature
; LOCATION: 1929
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; LOCATION: 2310
; OTHER INFORMATION: /note= "A is replaced by N for
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; OTHER INFORMATION: Wild-Type sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-1
Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAACGCGAGAGAAACCGCG 67

RESULT 8
PCT-US96-07627-2
; Sequence 2, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (DEN-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3381
; FEATURE:
```

```
; NAME/KEY: misc_feature
; LOCATION: 1216..1218
; OTHER INFORMATION: /note= "GAG(coding for Glu) is
; OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1258..1260
; OTHER INFORMATION: /note= "GTG(coding for Val) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: Strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1782..1784
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR15
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ([1])
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
; PCT-US96-07627-2
;
; Query Match 100.0%; Score 28; DB 5; Length 3381;
; Best Local Similarity 100.0%; Pred. No. 0.0029;
; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
; | | | | | | | | | | | | | | | | | | | |
; Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
;
; RESULT 9
; US-08-325-426B-1
; Sequence 1, Application US/08325426B
; Patent No. 6017535
```

```
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
; US-08-325-426B-1
;
; Query Match 94.3%; Score 26.4; DB 3; Length 10718;
; Best Local Similarity 96.4%; Pred. No. 0.02;
; Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
; | | | | | | | | | | | | | | | | | | | |
; Db 120 AATATGCTGAACCGGAGAGAAACCGCG 147
;
; RESULT 10
; US-09-270-767-9819/c
; Sequence 9819, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9819
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-9819
;
; Query Match 66.4%; Score 18.6; DB 4; Length 1145;
; Best Local Similarity 84.0%; Pred. No. 50;
; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

QY 2 ATATGCTGAAACGCGAGAGAAACCG 26
|||||
Db 452 ATATGCTGAAACGCGAGAGAAACCG 428

RESULT 11
US-09-078-173A-11
; Sequence 11, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Braah
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-09-078-173A-11

Query Match 65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 933 AAAATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 12
US-10-042-991-11
; Sequence 11, Application US/10042991
; Patent No. 6780621
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Braah
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match 65.7%; Score 18.4; DB 4; Length 1443;
Best Local Similarity 78.6%; Pred. No. 64;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 933 AAAATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 13
US-08-224-391-52
; Sequence 52, Application US/08224391
; Patent No. 5744140

; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-224-391-52

Query Match 65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 81;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 43 AATATGCTGAAACGCGGCTTATCCCGCG 70

RESULT 14
US-08-484-304-52
; Sequence 52, Application US/08484304
; Patent No. 5744141
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,304

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;
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-484-304-52
;
Query Match 65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 81;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGGAGAGAAACCGCG 28
Db 43 AATATGCTGAAACGCGGCTTACCCCGCG 70

RESULT 15
US-08-811-566-5/c
; Sequence 5, Application US/08811566
; Patent No. 6127116
; GENERAL INFORMATION:
; APPLICANT: Rice, Charles et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,566
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1113-1-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FILE REFERENCE: CL001307
```

```
US-08-811-566-5
;
Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGGAGAGAAACCGCG 28
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 16
US-09-034-756-5/c
; Sequence 5, Application US/09034756
; Patent No. 6392028
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-034-756-5
;
Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGGAGAGAAACCGCG 28
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 17
US-09-949-016-23984/c
; Sequence 23984, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23984
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23984

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 29 AAGATGCTGAAACGCGAGAGAAA 7

RESULT 18

US-09-949-016-91406/c
; Sequence 91406, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91406
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91406

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 104 AATATGCTGAATGCGATAAAA 82

RESULT 19

US-09-949-016-127192/c
; Sequence 127192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; SOFTWARE: FastSeq for Windows Version 4.0

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127192
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-127192

Query Match 65.0%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 29 AAGATGCTGAAACGCGAGAGAAA 7

RESULT 20

US-09-949-016-3621
; Sequence 3621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3621
; LENGTH: 3029
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3621

Query Match 65.0%; Score 18.2; DB 4; Length 3029;
Best Local Similarity 87.0%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||| ||||| ||||| ||||| |||||
Db 2399 AAGATGCTGAAACGCGAGAGAAA 2421

RESULT 21

US-09-949-016-295
; Sequence 295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

QY 1 AATATGCTGAACCGGAGAGAAA 23
|||||
Db 77034 AATATGCTGAATGCGGATAAAA 77012

RESULT 26

US-09-949-016-14513/c
; Sequence 14513, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14513
; LENGTH: 143173
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14513

Query Match .65.0%; Score 18.2; DB 4; Length 143173;
Best Local Similarity 87.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAA 23
|||||
Db 77043 AATATGCTGAATGCGGATAAAA 77021

RESULT 27

US-09-949-016-91405/c
; Sequence 91405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91405
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91405

Query Match .63.6%; Score 17.8; DB 4; Length 601;
Best Local Similarity 82.6%; Pred. No. 1e+02;
Matches 19; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAA 23
|||||
Db 315 AATATGCTGAATGCGGATAAAA 293

RESULT 28

US-09-830-433A-31/c
; Sequence 31, Application US/09830433A
; Patent No. 6835384
; GENERAL INFORMATION:
; APPLICANT: ALJAME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; strains of the Neisseria genus
; FILE REFERENCE: P07180US00/BAS
; CURRENT APPLICATION NUMBER: US/09/830,433A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(693)
US-09-830-433A-31

Query Match 62.9%; Score 17.6; DB 4; Length 696;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGCTGAACCGGAGAGAACCGCG 28
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Db 210 TGAAGAACCGCGCGGAAACCGCG 187

RESULT 29

US-09-583-110-2433
; Sequence 2433, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2433
; LENGTH: 3351
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2433

Query Match 62.9%; Score 17.6; DB 4; Length 3351;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAA 24
|||||
Db 830 AATATGCTGAGCTCTTGAGAAAC 853

RESULT 30

US-09-107-433-999
; Sequence 999, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

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; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC THERAPEUTICS
;
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 999:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3363 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...3363
; SEQUENCE DESCRIPTION: SEQ ID NO: 999:
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; US-09-107-433-999
;
; Query Match 62.9%; Score 17.6; DB 4; Length 3363;
; Best Local Similarity 83.3%; Pred. No. 1.8e+02;
; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGAGAGAAAC 24
; Db 842 AATATGCTGAAGCTCTTGAGAAAC 865
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; RESULT 31
; US-09-270-767-8086
; Sequence 8086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8086
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-8086
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Query Match 62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGAGAGAAACCGC 27
; Db 534 AATATCGAAACCGCGCAACAAACCGC 560
;
; RESULT 32
; US-09-270-767-23368
; Sequence 23368, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23368
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-23368
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Query Match 62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 1 AATATGCTGAACCGAGAGAAACCGC 27
; Db 534 AATATCGAAACCGCGCAACAAACCGC 560
;
; RESULT 33
; US-08-875-233-11
; Sequence 11, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell
; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; TITLE OF INVENTION: Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: WHITE LEAF
FEATURE:
NAME/KEY: CDS
LOCATION: 1..657
PUBLICATION INFORMATION:
AUTHORS: Quemada, H
AUTHORS: Kearney, C
AUTHORS: Gonsalves, D
AUTHORS: Slightom, J
TITLE: Nucleotide Sequences of the Coat Protein
TITLE: Genes and Flanking Regions of Cucumber Mosaic
TITLE: Virus Strains C and WL RNA 3
JOURNAL: J. Gen. Virol.
VOLUME: 70
PAGES: 1065-1073
DATE: 1989
US-08-875-233-11

Query Match 62.1%; Score 17.4; DB 3; Length 983;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACCGGAGAGAAACCGCG 28
DB 113 AGATGCTGAAACTCAATAGAACCTCG 139

RESULT 34
US-09-328-352-1888/c
Sequence 1888, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1888
LENGTH: 1227
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGGAGAGAAACCGCG 27
DB 964 AATATGCAAAACCGAAGAAACCGCG 938

RESULT 35
US-09-221-017B-558
Sequence 558, Application US/09221017B
Patent No. 644799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER

LENGTH: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PFI182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PFI546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PF2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NOS: 558:
SEQUENCE CHARACTERISTICS:
LENGTH: 2646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...2646
US-09-221-017B-558

Query Match 62.1%; Score 17.4; DB 3; Length 2646;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACCGGAGAGAAACCGCG 28
DB 1472 ACAGGATGAAAGCGAAGAAATCCGCG 1498

RESULT 36
US-09-549-872B-3
Sequence 3, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5026
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-3

Query Match 62.1%; Score 17.4; DB 4; Length 5026;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AAACGCGAGAGAAACCGCG 28
Db 2034 AAACGCGAGAGAAACCGCG 2052

RESULT 37
US-09-549-872B-5
; Sequence 5, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6612
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-5

Query Match 62.1%; Score 17.4; DB 4; Length 6612;
Best Local Similarity 94.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AAACGCGAGAGAAACCGCG 28
Db 2646 AAACGCGAGAGAAACCGCG 2664

RESULT 18
US-09-549-872B-2
; Sequence 2, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7

; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11207
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-2

Query Match 62.1%; Score 17.4; DB 4; Length 11207;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AAACGCGAGAGAAACCGCG 28
Db 2640 AAACGCGAGAGAAACCGCG 2658

RESULT 39
US-09-949-016-12428
; Sequence 12428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12428
; LENGTH: 45225
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12428

Query Match 62.1%; Score 17.4; DB 4; Length 45225;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
Db 23730 AGTCTGCTGAAACTGAAGAGAAACCCAC 23756

RESULT 40
US-09-949-016-12428/c
; Sequence 12428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12428
; LENGTH: 45225

;
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12428

Query Match 62.1%; Score 17.4; DB 4; Length 45225;
 Best Local Similarity 77.8%; Pred. No. 3.8e+02;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Search completed: July 31, 2005, 13:57:51
Job time : 99.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2005, 13:48:18 ; Search time 332.5 Seconds
(without alignments)
545.041 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatagctgaacgcgagagaacgcg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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23: /cgn2_6/prodata/1/pubpna/US11A_PUBCOMB.seq*
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26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	100.0	3381	16	US-10-247-960-2
3	28	100.0	10616	21	US-10-719-547-18
4	28	100.0	10649	21	US-10-719-547-14
5	28	100.0	10649	21	US-10-719-547-16
6	28	100.0	10724	19	US-10-699-550-4
7	28	100.0	15159	21	US-10-871-775-30

8	26.4	94.3	10735	19	US-10-699-550-3	Sequence 3, Appli
9	26	92.9	26	9	US-09-840-707A-23	Sequence 23, Appli
10	26	92.9	26	14	US-10-038-557A-23	Sequence 53, Appli
11	24.8	88.6	15053	21	US-10-871-775-32	Sequence 32, Appli
12	22	78.6	72	20	US-10-656-721-26	Sequence 26, Appli
13	19.6	70.0	594	20	US-10-425-115-108018	Sequence 108018,
14	19	67.9	765	20	US-10-363-345A-20593	Sequence 20593, A
15	19	67.9	765	20	US-10-363-345A-20594	Sequence 20594, A
16	19	67.9	765	21	US-10-363-483A-20593	Sequence 20593, A
17	19	67.9	765	21	US-10-363-483A-20594	Sequence 20594, A
18	18.8	67.1	1428	17	US-10-369-493-32952	Sequence 32952, A
19	18.6	66.4	1602	15	US-10-156-761-2266	Sequence 2266, Ap
20	18.6	66.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
21	18.4	65.7	1443	13	US-10-042-931-11	Sequence 11, Appli
22	18.4	65.7	12305	20	US-10-422-323A-2	Sequence 2, Appli
23	18.4	65.7	12315	20	US-10-422-323A-1	Sequence 1, Appli
24	18.4	65.7	12980	9	US-09-238-076-5	Sequence 5, Appli
25	18.4	65.7	12980	10	US-09-995-937-5	Sequence 5, Appli
26	18.4	65.7	12980	10	US-09-917-563-5	Sequence 5, Appli
27	18.2	65.0	25	21	US-10-719-900-399988	Sequence 399988,
28	18.2	65.0	452	10	US-09-918-995-27460	Sequence 27460, A
29	18.2	65.0	2179	9	US-09-823-245A-434	Sequence 434, App
30	18.2	65.0	3035	22	US-10-887-066-3	Sequence 3, Appli
31	18.2	65.0	9075	10	US-09-764-891-7878	Sequence 7878, Ap
32	17.6	62.9	529	18	US-10-424-539-130933	Sequence 130933,
33	17.6	62.9	550	14	US-10-198-846-11819	Sequence 11819, A
34	17.6	62.9	696	21	US-10-909-436-31	Sequence 31, Appli
35	17.6	62.9	838	14	US-10-198-846-3468	Sequence 3468, Ap
36	17.6	62.9	945	17	US-10-398-221-2508	Sequence 2508, Ap
37	17.6	62.9	945	17	US-10-398-221-2571	Sequence 2571, Ap
38	17.6	62.9	966	17	US-10-398-221-553	Sequence 553, App
39	17.6	62.9	966	17	US-10-398-221-554	Sequence 554, App
40	17.6	62.9	1646	17	US-10-282-122A-29374	Sequence 29374, A
41	17.6	62.9	3363	22	US-10-617-320-999	Sequence 999, App
42	17.6	62.9	9718	8	US-08-319-974A-1	Sequence 1, Appli
43	17.6	62.9	684707	17	US-10-398-221-9	Sequence 9, Appli
44	17.6	62.9	684707	17	US-10-398-221-9	Sequence 9, Appli
45	17.6	62.9	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
46	17.4	62.1	341	19	US-10-767-701-19049	Sequence 19049, A
47	17.4	62.1	379	10	US-09-738-269-20	Sequence 20, Appli
48	17.4	62.1	379	13	US-10-023-437-20	Sequence 20, Appli
49	17.4	62.1	382	19	US-10-437-963-17200	Sequence 17200, A
50	17.4	62.1	528	18	US-10-424-539-53946	Sequence 53946, A
51	17.4	62.1	558	13	US-10-027-632-237136	Sequence 237136,
52	17.4	62.1	558	17	US-10-027-632-237136	Sequence 237136,
53	17.4	62.1	589	20	US-10-363-345A-34197	Sequence 34197, A
54	17.4	62.1	589	20	US-10-363-345A-34198	Sequence 34198, A
55	17.4	62.1	589	21	US-10-363-483A-34198	Sequence 34198, A
56	17.4	62.1	589	21	US-10-363-483A-34198	Sequence 34198, A
57	17.4	62.1	691	20	US-10-363-345A-38631	Sequence 38631, A
58	17.4	62.1	691	20	US-10-363-345A-38632	Sequence 38632, A
59	17.4	62.1	691	21	US-10-363-483A-38631	Sequence 38631, A
60	17.4	62.1	691	21	US-10-363-483A-38632	Sequence 38632, A
61	17.4	62.1	774	17	US-10-282-122A-39862	Sequence 39862, A
62	17.4	62.1	778	17	US-10-282-122A-39862	Sequence 39862, A
63	17.4	62.1	983	13	US-10-011-033-11	GENERAL INFORMA
64	17.4	62.1	2520	10	US-09-738-269-22	Sequence 22, Appli
65	17.4	62.1	2520	13	US-10-023-437-22	Sequence 22, Appli
66	17.4	62.1	2646	13	US-10-194-163-558	Sequence 558, App
67	17.4	62.1	2784	19	US-10-437-963-21921	Sequence 21921, A
68	17.4	62.1	5026	15	US-10-371-101-3	Sequence 3, Appli
69	17.4	62.1	6612	15	US-10-371-101-5	Sequence 5, Appli
70	17.4	62.1	11207	15	US-10-371-101-2	Sequence 2, Appli
71	17.4	62.1	39726	16	US-10-309-933-1	Sequence 1, Appli
72	17.4	62.1	115780	19	US-10-367-094-96	Sequence 96, Appli
73	17.4	62.1	145068	19	US-10-322-281-33	Sequence 33, Appli
74	17.4	62.1	235070	13	US-10-087-192-1990	Sequence 1990, Ap
75	17.2	61.4	600	22	US-10-972-079-1314	Sequence 1314, Ap
76	17.2	61.4	1428	17	US-10-369-493-33163	Sequence 33163, A
77	17.2	61.4	1506	17	US-10-369-493-41224	Sequence 41224, A
78	17.2	61.4	1589	19	US-10-767-701-15529	Sequence 15529, A
79	17.2	61.4	1960	9	US-09-834-975-833	Sequence 833, App
80	17.2	61.4	1960	20	US-10-357-930-22162	Sequence 22162, A

81	17.2	61.4	1960	20	US-10-357-930-28023	Sequence 28023, A	c 154	16.8	60.0	1654	19	US-10-767-795-6416	Sequence 6416, Ap
82	17.2	61.4	1960	20	US-10-357-930-28979	Sequence 28979, A	155	16.8	60.0	1657	17	US-10-398-221-3320	Sequence 3320, Ap
83	17.2	61.4	3201	19	US-10-664-705-152	Sequence 152, App	c 156	16.8	60.0	1666	18	US-10-424-599-52031	Sequence 52031, A
c 84	17.2	61.4	3477	19	US-10-437-963-14564	Sequence 14564, A	157	16.8	60.0	2219	18	US-10-425-114-31393	Sequence 31393, A
85	17.2	61.4	3639	19	US-10-437-963-14560	Sequence 14560, A	158	16.8	60.0	2261	17	US-10-282-122A-29289	Sequence 29289, A
86	17.2	61.4	24358	16	US-10-369-978-1	Sequence 1, Appl1	159	16.8	60.0	3210	17	US-10-374-780A-1609	Sequence 1609, Ap
c 87	17.2	61.4	2731748	19	US-10-297-465A-1	Sequence 1, Appl1	160	16.8	60.0	3210	18	US-10-412-693B-1658	Sequence 1658, Ap
c 88	17	60.7	417	9	US-09-770-423-444	Sequence 444, App	c 161	16.8	60.0	3222	19	US-10-437-963-1658	Sequence 3736, Ap
c 89	17	60.7	437	9	US-09-960-352-2523	Sequence 2523, Ap	162	16.8	60.0	3350	20	US-10-425-115-109187	Sequence 109187,
c 90	17	60.7	516	13	US-10-027-632-51441	Sequence 51441, A	c 163	16.8	60.0	3351	19	US-10-437-963-3741	Sequence 3741, Ap
c 91	17	60.7	516	17	US-10-027-632-51441	Sequence 51441, A	c 164	16.8	60.0	3720	19	US-10-437-963-3735	Sequence 3735, Ap
c 92	17	60.7	520	13	US-10-027-632-248635	Sequence 248635, A	c 165	16.8	60.0	5064	19	US-10-437-963-85044	Sequence 85044, A
c 93	17	60.7	520	17	US-10-027-632-248635	Sequence 248635, A	166	16.8	60.0	5064	19	US-09-764-891-8362	Sequence 8362, Ap
c 94	17	60.7	565	13	US-10-027-632-83075	Sequence 83075, A	167	16.8	60.0	5965	15	US-10-764-891-8362	Sequence 787, App
95	17	60.7	565	13	US-10-027-632-83075	Sequence 83075, A	168	16.8	60.0	10945	15	US-10-205-428-787	Sequence 787, App
96	17	60.7	565	17	US-10-027-632-83075	Sequence 83075, A	169	16.8	60.0	10945	19	US-10-361-002-5	Sequence 5, Appl1
97	17	60.7	565	17	US-10-027-632-83075	Sequence 83075, A	170	16.8	60.0	10975	19	US-10-361-004-5	Sequence 5, Appl1
98	17	60.7	661	20	US-10-027-632-315971	Sequence 315971, A	171	16.8	60.0	11029	19	US-10-698-550-1	Sequence 1, Appl1
99	17	60.7	835	13	US-10-027-632-157206	Sequence 157206, A	172	16.8	60.0	11029	21	US-10-698-550-2	Sequence 2, Appl1
100	17	60.7	835	17	US-10-027-632-157206	Sequence 157206, A	173	16.8	60.0	11029	21	US-10-679-520A-66	Sequence 66, Appl1
c 101	17	60.7	14000	21	US-10-893-671-1	Sequence 1, Appl1	174	16.8	60.0	11029	22	US-10-706-892-1	Sequence 1, Appl1
c 102	17	60.7	28953	20	US-10-719-993-6811	Sequence 6811, Ap	175	16.8	60.0	11029	22	US-10-706-892-2	Sequence 2, Appl1
c 103	17	60.7	163701	19	US-10-322-281-439	Sequence 439, App	176	16.8	60.0	12790	21	US-10-985-805-1	Sequence 1, Appl1
c 104	17	60.7	227931	17	US-10-085-117-274	Sequence 274, App	c 177	16.8	60.0	38234	13	US-10-087-192-1762	Sequence 1762, Ap
105	17	60.7	1601042	13	US-10-027-632-59064	Sequence 59064, A	178	16.8	60.0	59514	19	US-10-322-696-112	Sequence 584, App
c 106	17	60.7	1601042	17	US-10-027-632-59064	Sequence 59064, A	c 179	16.8	60.0	188794	19	US-10-322-696-112	Sequence 112, App
c 107	16.8	60.0	69	20	US-10-688-489-16	Sequence 16, Appl	180	16.6	59.3	25	21	US-10-719-900-399987	Sequence 399987,
c 108	16.8	60.0	366	20	US-10-425-115-135770	Sequence 135770, A	181	16.6	59.3	34	22	US-10-957-433-56	Sequence 56, Appl
c 109	16.8	60.0	421	20	US-10-425-115-135770	Sequence 135770, A	182	16.6	59.3	201	20	US-10-425-115-111057	Sequence 111057,
c 110	16.8	60.0	503	20	US-10-363-345A-17699	Sequence 17699, A	c 183	16.6	59.3	404	18	US-10-424-599-6683	Sequence 6683, Ap
c 111	16.8	60.0	503	20	US-10-363-345A-17699	Sequence 17699, A	184	16.6	59.3	409	19	US-10-469-285-701	Sequence 701, App
c 112	16.8	60.0	503	21	US-10-363-483A-17700	Sequence 17700, A	185	16.6	59.3	447	15	US-10-002-632-531	Sequence 531, App
c 113	16.8	60.0	503	21	US-10-363-483A-17700	Sequence 17700, A	186	16.6	59.3	487	21	US-10-487-901-6807	Sequence 6807, Ap
c 114	16.8	60.0	509	20	US-10-363-483A-17700	Sequence 17700, A	187	16.6	59.3	504	16	US-10-029-386-7986	Sequence 7986, Ap
c 115	16.8	60.0	509	20	US-10-363-483A-17700	Sequence 17700, A	c 188	16.6	59.3	570	13	US-10-029-386-7986	Sequence 51307, A
c 116	16.8	60.0	509	21	US-10-363-483A-17700	Sequence 17700, A	c 189	16.6	59.3	570	13	US-10-027-632-51307	Sequence 51308, A
c 117	16.8	60.0	509	21	US-10-363-483A-17700	Sequence 17700, A	c 190	16.6	59.3	570	13	US-10-027-632-51308	Sequence 51309, A
c 118	16.8	60.0	517	20	US-10-425-115-82733	Sequence 82733, A	c 191	16.6	59.3	570	13	US-10-027-632-51309	Sequence 51310, A
c 119	16.8	60.0	556	18	US-10-424-599-52030	Sequence 52030, A	c 192	16.6	59.3	570	17	US-10-027-632-51307	Sequence 51307, A
c 120	16.8	60.0	569	18	US-10-424-599-52030	Sequence 52030, A	c 193	16.6	59.3	570	17	US-10-027-632-51308	Sequence 51308, A
c 121	16.8	60.0	599	22	US-10-972-079-63395	Sequence 63395, A	c 194	16.6	59.3	570	17	US-10-027-632-51309	Sequence 51309, A
c 122	16.8	60.0	620	20	US-10-425-115-145285	Sequence 145285, A	c 195	16.6	59.3	575	20	US-10-425-115-76549	Sequence 76549, A
c 123	16.8	60.0	621	9	US-09-764-846-105	Sequence 105, App	196	16.6	59.3	600	22	US-10-972-079-19196	Sequence 19196, A
c 124	16.8	60.0	621	14	US-10-091-483-105	Sequence 105, App	c 197	16.6	59.3	680	18	US-10-425-114-8764	Sequence 8764, Ap
c 125	16.8	60.0	634	13	US-10-027-632-6272	Sequence 6272, Ap	198	16.6	59.3	680	20	US-10-425-114-8764	Sequence 8764, Ap
c 126	16.8	60.0	634	17	US-10-027-632-6272	Sequence 6272, Ap	c 199	16.6	59.3	689	20	US-10-425-115-20769	Sequence 20769, A
c 127	16.8	60.0	699	21	US-10-487-901-2868	Sequence 2868, Ap	200	16.6	59.3	702	8	US-08-781-986A-314	Sequence 314, App
c 128	16.8	60.0	711	18	US-10-424-599-58144	Sequence 58144, A	201	16.6	59.3	702	18	US-10-329-624-314	Sequence 314, App
c 129	16.8	60.0	716	20	US-10-363-345A-26673	Sequence 26673, A	202	16.6	59.3	707	20	US-10-425-115-20775	Sequence 20775, A
c 130	16.8	60.0	716	20	US-10-363-345A-26674	Sequence 26674, A	203	16.6	59.3	761	20	US-10-425-115-20768	Sequence 20768, A
c 131	16.8	60.0	716	21	US-10-363-483A-26673	Sequence 26673, A	c 204	16.6	59.3	770	20	US-10-425-115-167404	Sequence 167404, A
c 132	16.8	60.0	716	21	US-10-363-483A-26674	Sequence 26674, A	205	16.6	59.3	804	18	US-10-425-114-15623	Sequence 15623, A
c 133	16.8	60.0	725	17	US-10-027-632-18419	Sequence 18419, A	814	16.6	59.3	814	13	US-10-027-632-170035	Sequence 170035, A
c 134	16.8	60.0	725	17	US-10-027-632-18419	Sequence 18419, A	814	16.6	59.3	814	13	US-10-027-632-170036	Sequence 170036, A
c 135	16.8	60.0	788	20	US-10-363-345A-7386	Sequence 7386, Ap	814	16.6	59.3	814	17	US-10-027-632-170035	Sequence 170035, A
c 136	16.8	60.0	788	20	US-10-363-345A-7386	Sequence 7386, Ap	829	16.6	59.3	829	21	US-10-472-928-623	Sequence 623, App
c 137	16.8	60.0	788	21	US-10-363-483A-7385	Sequence 7385, Ap	831	16.6	59.3	831	21	US-10-472-928-623	Sequence 623, App
c 138	16.8	60.0	788	21	US-10-363-483A-7386	Sequence 7386, Ap	841	16.6	59.3	841	18	US-10-472-928-623	Sequence 623, App
c 139	16.8	60.0	857	20	US-10-363-345A-29811	Sequence 29811, A	851	16.6	59.3	851	8	US-08-961-527-361	Sequence 132044, A
c 140	16.8	60.0	857	20	US-10-363-345A-29812	Sequence 29812, A	851	16.6	59.3	851	17	US-10-158-844-361	Sequence 361, App
c 141	16.8	60.0	857	21	US-10-363-483A-29811	Sequence 29811, A	895	16.6	59.3	895	17	US-10-425-114-22161	Sequence 22161, A
c 142	16.8	60.0	857	21	US-10-363-483A-29812	Sequence 29812, A	923	16.6	59.3	923	18	US-10-282-122A-35207	Sequence 35207, A
c 143	16.8	60.0	906	17	US-10-282-122A-29547	Sequence 29547, A	923	16.6	59.3	923	18	US-10-425-114-18889	Sequence 18889, A
c 144	16.8	60.0	996	18	US-10-425-114-34006	Sequence 34006, A	968	16.6	59.3	968	20	US-10-425-114-23881	Sequence 23881, A
c 145	16.8	60.0	1078	20	US-10-424-599-73696	Sequence 73696, A	c 977	16.6	59.3	977	20	US-10-739-930-850	Sequence 850, App
c 146	16.8	60.0	1172	20	US-10-425-115-109185	Sequence 109185, A	993	16.6	59.3	993	18	US-10-425-115-135677	Sequence 135677, A
c 147	16.8	60.0	1179	20	US-10-363-345A-16665	Sequence 16665, A	1034	16.6	59.3	1034	18	US-10-425-114-82	Sequence 82, Appl
c 148	16.8	60.0	1179	21	US-10-363-345A-16666	Sequence 16666, A	1058	16.6	59.3	1058	21	US-10-425-114-82	Sequence 82, Appl
c 149	16.8	60.0	1179	21	US-10-363-483A-16665	Sequence 16665, A	1088	16.6	59.3	1088	21	US-10-424-599-132042	Sequence 132042, A
c 150	16.8	60.0	1257	17	US-10-363-483A-16666	Sequence 16666, A	1088	16.6	59.3	1088	21	US-10-487-901-3076	Sequence 3076, Ap
c 151	16.8	60.0	1257	17	US-10-282-122A-9259	Sequence 9259, App	1078	16.6	59.3	1078	20	US-10-487-901-6811	Sequence 6811, Ap
c 152	16.8	60.0	1289	17	US-10-369-493-40219	Sequence 40219, A	1141	16.6	59.3	1141	13	US-10-425-115-140548	Sequence 140548, A
c 153	16.8	60.0	1382	20	US-10-739-930-466	Sequence 466, App	1141	16.6	59.3	1141	13	US-10-027-632-118252	Sequence 118252, A

227	16.6	59.3	1141	17	US-10-027-632-118252	Sequence 118252,	300	16.4	58.6	675	18	US-10-424-599-84542	Sequence 84542, A
228	16.6	59.3	1191	21	US-10-487-901-4566	Sequence 4566, Ap	301	16.4	58.6	682	9	US-09-770-149-337	Sequence 337, App
229	16.6	59.3	1200	17	US-10-282-122A-8017	Sequence 8017, Ap	c 302	16.4	58.6	742	21	US-10-494-672-345	Sequence 345, App
230	16.6	59.3	1221	20	US-10-363-345A-28151	Sequence 28151, A	303	16.4	58.6	768	14	US-09-777-564-529	Sequence 529, App
231	16.6	59.3	1221	20	US-10-363-345A-28151	Sequence 28152, A	304	16.4	58.6	768	14	US-10-015-219-529	Sequence 529, App
232	16.6	59.3	1221	21	US-10-363-483A-28151	Sequence 28151, A	305	16.4	58.6	849	17	US-10-027-632-9181	Sequence 9181, Ap
233	16.6	59.3	1221	21	US-10-363-483A-28151	Sequence 28152, A	306	16.4	58.6	849	17	US-10-027-632-9181	Sequence 9181, Ap
234	16.6	59.3	1223	20	US-10-363-345A-31157	Sequence 31157, A	c 307	16.4	58.6	988	20	US-10-363-345A-33881	Sequence 33881, A
235	16.6	59.3	1223	20	US-10-363-345A-31158	Sequence 31158, A	308	16.4	58.6	988	20	US-10-363-345A-33882	Sequence 33882, A
236	16.6	59.3	1223	21	US-10-363-483A-31157	Sequence 31157, A	c 309	16.4	58.6	988	21	US-10-363-483A-33881	Sequence 33881, A
237	16.6	59.3	1223	21	US-10-363-483A-31158	Sequence 31158, A	310	16.4	58.6	988	21	US-10-363-483A-33882	Sequence 33882, A
238	16.6	59.3	1399	18	US-10-424-599-25204	Sequence 25204, A	c 311	16.4	58.6	1029	17	US-10-369-493-31372	Sequence 31372, A
239	16.6	59.3	1584	17	US-10-282-122A-11840	Sequence 11840, A	c 312	16.4	58.6	1051	20	US-10-425-115-148939	Sequence 148939, A
240	16.6	59.3	1682	19	US-10-437-963-72027	Sequence 72027, A	c 313	16.4	58.6	1069	20	US-10-425-115-148939	Sequence 148939, A
241	16.6	59.3	1704	17	US-10-369-493-34563	Sequence 34563, A	c 314	16.4	58.6	1137	17	US-10-437-963-72027	Sequence 72027, A
242	16.6	59.3	1974	17	US-10-369-493-40787	Sequence 40787, A	c 315	16.4	58.6	1404	17	US-10-437-963-72027	Sequence 72027, A
243	16.6	59.3	2000	17	US-10-260-238-2159	Sequence 2159, Ap	c 316	16.4	58.6	1404	17	US-10-437-963-72027	Sequence 72027, A
244	16.6	59.3	2558	9	US-09-939-980-214	Sequence 214, App	c 317	16.4	58.6	1455	9	US-09-738-626-2886	Sequence 2886, Ap
245	16.6	59.3	2666	9	US-09-853-386-2	Sequence 2, Appli	c 318	16.4	58.6	1568	18	US-10-424-599-58090	Sequence 58090, A
246	16.6	59.3	2666	15	US-10-205-951-44	Sequence 44, Appl	c 319	16.4	58.6	1568	18	US-10-424-599-58090	Sequence 58090, A
247	16.6	59.3	3636	9	US-09-815-242-4224	Sequence 4224, Ap	c 320	16.4	58.6	1578	18	US-10-450-555-29	Sequence 29, Appl
248	16.6	59.3	4079	18	US-10-424-599-67519	Sequence 67519, A	c 321	16.4	58.6	1687	20	US-10-739-930-1658	Sequence 1658, Ap
249	16.6	59.3	4449	9	US-09-815-242-8386	Sequence 8386, Ap	c 322	16.4	58.6	1790	20	US-10-425-115-49071	Sequence 49071, A
250	16.6	59.3	4594	9	US-09-070-927A-230	Sequence 230, App	c 323	16.4	58.6	1840	19	US-10-437-963-85824	Sequence 85824, A
251	16.6	59.3	9372	16	US-10-293-582-2	Sequence 2, Appli	c 324	16.4	58.6	2354	18	US-10-424-599-125516	Sequence 125516, A
252	16.6	59.3	9372	21	US-10-956-157-1285	Sequence 1285, Ap	c 325	16.4	58.6	2369	9	US-09-895-382-29	Sequence 29, Appl
253	16.6	59.3	25685	21	US-10-292-798-709	Sequence 709, App	c 326	16.4	58.6	2778	19	US-10-437-963-36035	Sequence 36035, A
254	16.6	59.3	134841	13	US-10-087-193-1387	Sequence 1987, Ap	c 327	16.4	58.6	3010	20	US-10-801-847-1	Sequence 1, Appli
255	16.6	59.3	143899	10	US-09-873-319-3329	Sequence 15, Appl	c 328	16.4	58.6	3010	20	US-10-801-847-1	Sequence 1, Appli
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257	16.6	59.3	152759	21	US-10-322-281-10	Sequence 10, Appl	c 330	16.4	58.6	3128	14	US-10-198-846-9988	Sequence 9988, Ap
258	16.6	59.3	401433	22	US-10-737-082-79	Sequence 79, Appl	c 331	16.4	58.6	3797	20	US-10-425-115-148938	Sequence 148938, A
259	16.6	59.3	401433	22	US-10-737-082-79	Sequence 79, Appl	c 332	16.4	58.6	3870	15	US-10-225-567A-143	Sequence 143, App
260	16.6	59.3	2162598	21	US-10-472-928-4979	Sequence 4979, Ap	c 333	16.4	58.6	3870	15	US-10-225-567A-143	Sequence 143, App
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264	16.4	58.6	214	9	US-09-880-107-1805	Sequence 1805, Ap	c 337	16.4	58.6	6050	15	US-10-172-086-49	Sequence 49, Appl
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267	16.4	58.6	316	17	US-10-369-493-30337	Sequence 30337, A	c 340	16.4	58.6	6050	20	US-10-480-846-49	Sequence 49, Appl
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269	16.4	58.6	390	9	US-09-738-626-692	Sequence 692, App	c 342	16.4	58.6	6235	15	US-10-311-455-759	Sequence 759, Ap
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271	16.4	58.6	504	20	US-10-363-345A-17145	Sequence 17145, A	c 344	16.4	58.6	7309	18	US-10-221-714A-289	Sequence 289, App
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276	16.4	58.6	600	22	US-10-972-079-84546	Sequence 84546, A	c 349	16.4	58.6	13606	18	US-10-240-453-188	Sequence 188, App
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279	16.4	58.6	605	13	US-10-027-632-191203	Sequence 191203, A	c 352	16.4	58.6	175590	10	US-09-911-077A-13	Sequence 13, Appl
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291	16.4	58.6	630	9	US-09-777-564-1701	Sequence 1701, Ap	c 364	16.4	58.6	175590	10	US-09-911-077A-13	Sequence 13, Appl
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295	16.4	58.6	652	20	US-10-363-345A-18311	Sequence 18311, A	c 368	16.4	58.6	175590	10	US-09-911-077A-13	Sequence 13, Appl
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381	16.2	57.9	537	14	US-10-040-862-8874	Sequence 8874, Ap	454	16	57.1	296	14	US-10-060-036-3038	Sequence 3038, Ap
382	16.2	57.9	537	17	US-10-057-475B-8874	Sequence 8874, Ap	455	16	57.1	365	20	US-10-425-115-85477	Sequence 85477, A
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c 427	16.2	57.9	3747	17	US-10-399-214-17	Sequence 17, Appl	c 500	16	57.1	700	20	US-10-739-930-236	Sequence 236, App
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c 438	16.2	57.9	7042	9	US-09-876-667-15	Sequence 15, Appl							
c 439	16.2	57.9	9696	18	US-10-052-482-10	Sequence 10, Appl							
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c 444	16.2	57.1	20	21	US-10-913-996-6	Sequence 6, Appli							
c 445	16.2	57.1	20	21	US-10-913-996-17	Sequence 17, Appl							

ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2

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; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-085-944-2

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RESULT 2
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; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Coller, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

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RESULT 3
US-10-719-547-18
; Sequence 18, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/719,547
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Dengue 4 virus strain 2A
US-10-719-547-14

Query Match      100.0%; Score 28; DB 21; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
    |||||

RESULT 4
US-10-719-547-14
; Sequence 14, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Dengue 4 virus strain 2A
US-10-719-547-14

Query Match      100.0%; Score 28; DB 21; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
    |||||
Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165
    |||||

RESULT 5
US-10-719-547-16
; Sequence 16, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
```

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; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Recombinant Dengue 4 virus strain rDEN4
US-10-719-547-16

Query Match      100.0%; Score 28; DB 21; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 138 AATATGCTGAAACCGGAGAGAAACCGCG 165

RESULT 6
US-10-699-550-4
; Sequence 4, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
US-10-699-550-4

Query Match      100.0%; Score 28; DB 19; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

RESULT 7
US-10-871-775-30
; Sequence 30, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775

; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10649
; TYPE: DNA
; ORGANISM: Recombinant Dengue 4 virus strain rDEN4
US-10-719-547-16

Query Match      100.0%; Score 28; DB 21; Length 10649;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 138 AATATGCTGAAACCGGAGAGAAACCGCG 165

RESULT 6
US-10-699-550-4
; Sequence 4, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
US-10-699-550-4

Query Match      100.0%; Score 28; DB 19; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

RESULT 7
US-10-871-775-30
; Sequence 30, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775

; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US03/00594
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,281
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 15159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dengue2 (Tonga/74) plaemid p2
US-10-871-775-30

Query Match      100.0%; Score 28; DB 21; Length 15159;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 136 AATATGCTGAAACCGGAGAGAAACCGCG 163

RESULT 8
US-10-699-550-3
; Sequence 3, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10735
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-699-550-3

Query Match      94.3%; Score 26.4; DB 19; Length 10735;
Best Local Similarity 96.4%; Pred. No. 0.092;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACCGGAGAGAAACCGCG 28
    |||||
Db 134 AATATGCTGAAACCGGAGAGAAACCGCG 161

RESULT 9
US-09-840-707A-23
; Sequence 23, Application US/09840707A
; Patent No. US20020077276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
```

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; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-09-840-707A-23

Query Match          92.9%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCG 26
   ||||||||||||||||||||||||||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 10
US-10-038-557A-23
; Sequence 23, Application US/10038557A
; Publication No. US20030092684A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301D
; CURRENT APPLICATION NUMBER: US/10/038,557A
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/840,707
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23

Query Match          92.9%; Score 26; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCG 26
   ||||||||||||||||||||||||||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 11
US-10-871-775-32
; Sequence 32, Application US/10871775
; Publication No. US20050100886A1
; GENERAL INFORMATION:
; APPLICANT: Pletnev, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
```

```
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; TITLE OF INVENTION: PREVENT DISEASE CAUSED BY WEST NILE VIRUS.
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US03/00594
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,281
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 15053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dengue 3 (Sleman/78) plasmid p3
US-10-871-775-32

Query Match          88.6%; Score 24.8; DB 21; Length 15053;
Best Local Similarity 92.9%; Pred. No. 0.5;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
   ||||||||||||||||||||||||||||
Db 134 AATATGCTGAAACGCGTGTGAGAAACCGTG 161

RESULT 12
US-10-656-721-26
; Sequence 26, Application US/10656721
; Publication No. US20040265338A1
; GENERAL INFORMATION:
; APPLICANT: Pang, Xiaowu
; APPLICANT: Dayton, Andrew I.
; APPLICANT: Zhang, Minglie
; TITLE OF INVENTION: SURGENOMIC REPLICONS OF THE FLAVIVIRUS
; TITLE OF INVENTION: DENGUE
; FILE REFERENCE: NIH202.001C1
; CURRENT APPLICATION NUMBER: US/10/656,721
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/US02/06962
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/274,684
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' primer
US-10-656-721-26

Query Match          78.6%; Score 22; DB 20; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAA 22
   ||||||||||||||||||||||||
Db 28 AATATGCTGAAACGCGAGAGAA 49

RESULT 13
US-10-425-115-108018
; Sequence 108018, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
```


Query Match 67.9%; Score 19; DB 21; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 441 ATACGCGAAACGCGAAGAAACCGCG 467

RESULT 18
US-10-369-493-32952/c
; Sequence 32952, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 32952
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-369-493-32952

Query Match 67.1%; Score 18.8; DB 17; Length 1428;
Best Local Similarity 90.3%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAAACGCGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 1184 CGGAACGCGAGAGAAACCGCG 1163

RESULT 19
US-10-156-761-2286
; Sequence 2286, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2286
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1602)
US-10-156-761-2286

Query Match 66.4%; Score 18.6; DB 15; Length 1602;

Best Local Similarity 84.0%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGAAACGCGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 115 AAGCTGCACCGCGAGAGCAACCGCG 139

RESULT 20
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 66.4%; Score 18.6; DB 15; Length 9025608;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 ATGCTGAAACGCGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 2778649 AAGCTGCACCGCGAGAGCAACCGCG 2778625

RESULT 21
US-10-042-991-11
; Sequence 11, Application US/10042991
; Publication No. US20020142407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIMUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.000103
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match 65.7%; Score 18.4; DB 13; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.9e+02;

Qy	1	AATATGCTGAACCGCGAGAAACCGCG	28
Db	9209	AATATGCTAAAAACCGCGCATACCCCGC	9182


```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,937
; FILING DATE: 28-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-995-937-5

Query Match 65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGCGAGAGAAACCGCG 28
Db 9714 AATATGCTGAAACGGCGAGAGAAACCGCG 9687

RESULT 26
US-09-917-563-5/C
; Sequence 5, Application US/09917563
; Publication No. US20030073080A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,563
; FILING DATE: 27-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/238,076
; FILING DATE: 26-JAN-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-917-563-5

Query Match 65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGCGAGAGAAACCGCG 28
Db 9714 AATATGCTGAAACGGCGAGAGAAACCGCG 9687

RESULT 27
US-10-719-900-399988/C
; Sequence 399988, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 399988
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-399988

Query Match 65.0%; Score 18.2; DB 21; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGCGAGAGAAA 23
Db 24 AATTTGCTGAAACCGGAGAGAAA 2

RESULT 28
US-09-918-995-27460
; Sequence 27460, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27460
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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RESULT 33

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US-10-198-846-11819/c
; Sequence 11819, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11819
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 506, 549, 550
; OTHER INFORMATION: n = A, T, C or G
US-10-198-846-11819
Query Match 62.9%; Score 17.6; DB 14; Length 550;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAAC 24
Db 45 AATTTGCGGAACCTGGAGAGAAAC 22
RESULT 34
US-10-909-436-31/c
; Sequence 31, Application US/10909436
; Publication No. US20050032103A1
; GENERAL INFORMATION:
; APPLICANT: AUJME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; TITLE OF INVENTION: strains of the Neisseria genus
; FILE REFERENCE: P07180US00/BAS
; CURRENT APPLICATION NUMBER: US/10/909,436
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; NAME/KEY: CDS
; LOCATION: (1)..(693)
US-10-909-436-31
Query Match 62.9%; Score 17.6; DB 21; Length 696;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 TGCTGAAACGCGAGAGAAACCGG 28
Db 210 TGAAGAAACGCGGCGGAAACCGG 187
RESULT 35
US-10-198-846-3468/c
; Sequence 3468, Application US/10198846
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; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3468
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 557, 616, 641, 691, 749, 765, 796, 798, 815, 821
; OTHER INFORMATION: n = A, T, C or G
US-10-198-846-3468
Query Match 62.9%; Score 17.6; DB 14; Length 838;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAAC 24
Db 108 AATTTGCGGAACCTGGAGAGAAAC 85
RESULT 36
US-10-398-221-2508
; Sequence 2508, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2508
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2508
Query Match 62.9%; Score 17.6; DB 17; Length 945;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 TATGCTGAAACGCGAGAGAAACCG 26
Db 193 TATGCTGAAACACATGAGAGAAACAG 216
RESULT 37
US-10-398-221-2571
; Sequence 2571, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
```

```
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2571
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-5571

Query Match      62.9%; Score 17.6; DB 17; Length 945;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
    |||||
Db 193 TATGCTGAACACATGAGAAACAG 216

RESULT 38
US-10-398-221-553
; Sequence 553, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 553
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-553

Query Match      62.9%; Score 17.6; DB 17; Length 966;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
    |||||
Db 214 TATGCTGAACACATGAGAAACAG 237

RESULT 39
US-10-398-221-554
; Sequence 554, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 554
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-554

Query Match      62.9%; Score 17.6; DB 17; Length 966;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TATGCTGAACGCGAGAGAAACCG 26
    |||||
Db 214 TATGCTGAACACATGAGAAACAG 237

US-10-282-122A-29374/c
; Sequence 29374, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29374
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-282-122A-29374

Query Match      62.9%; Score 17.6; DB 17; Length 1646;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TGCTGAACGCGAGAGAAACCG 28
    |||||
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Db 210 TGAAGAAACGGCGGGAAACCGCG 187

Search completed: July 31, 2005, 15:46:25
Job time : 367.5 secs

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